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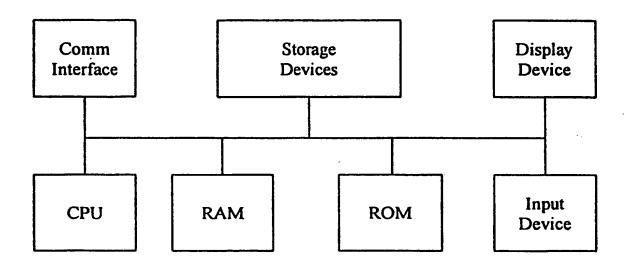
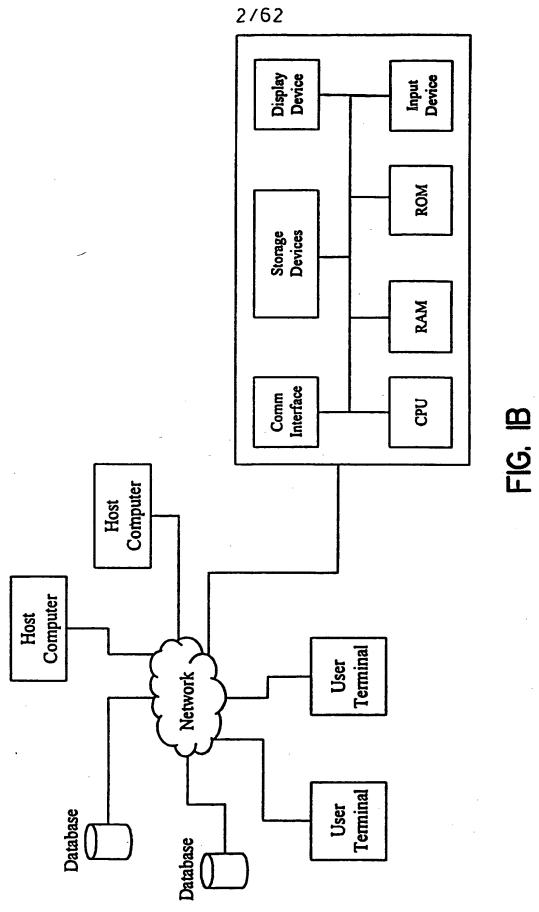


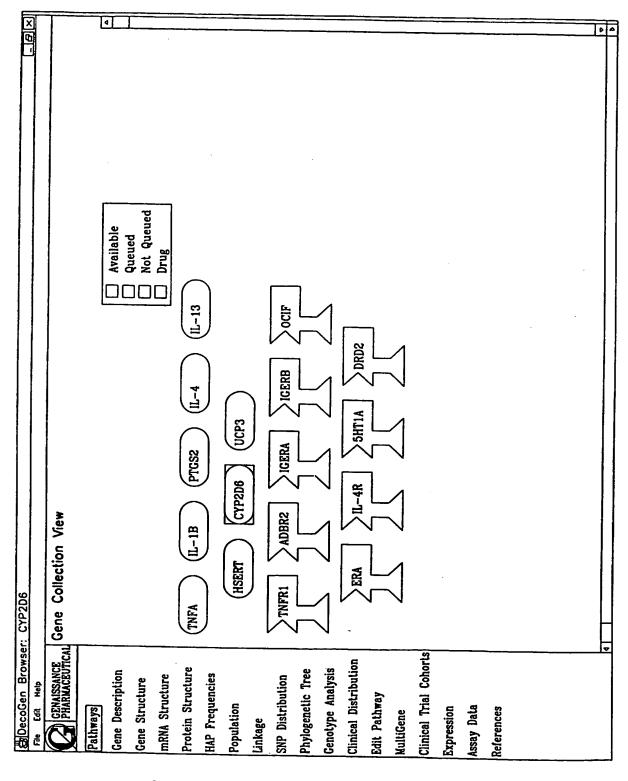
FIG. IA



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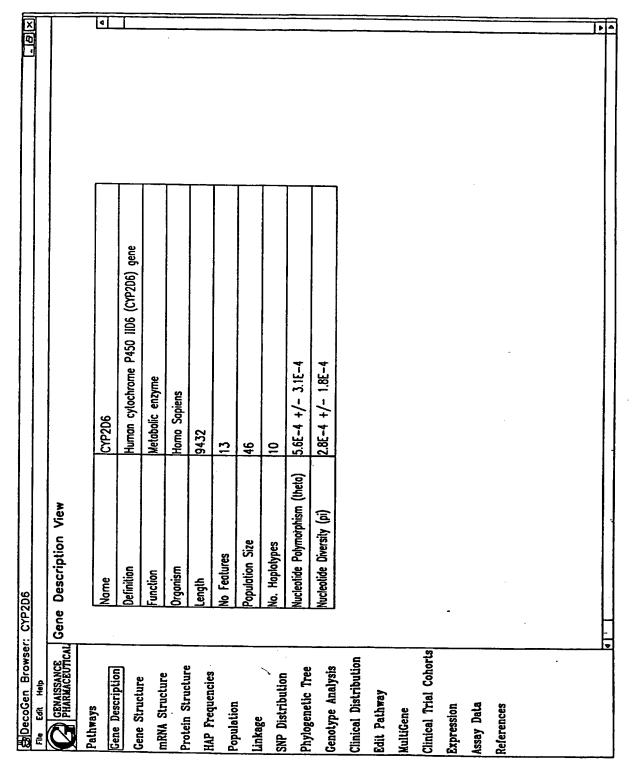
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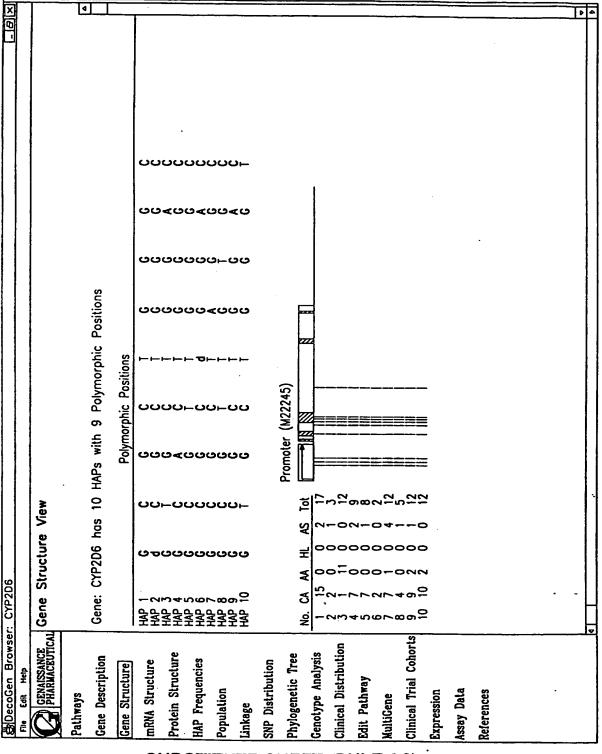
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**FIG** 

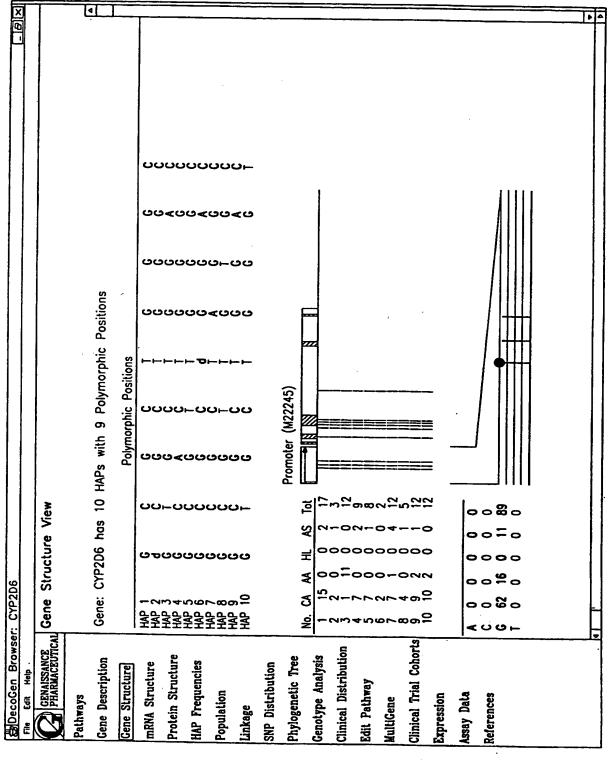


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FIG. 4b (2)



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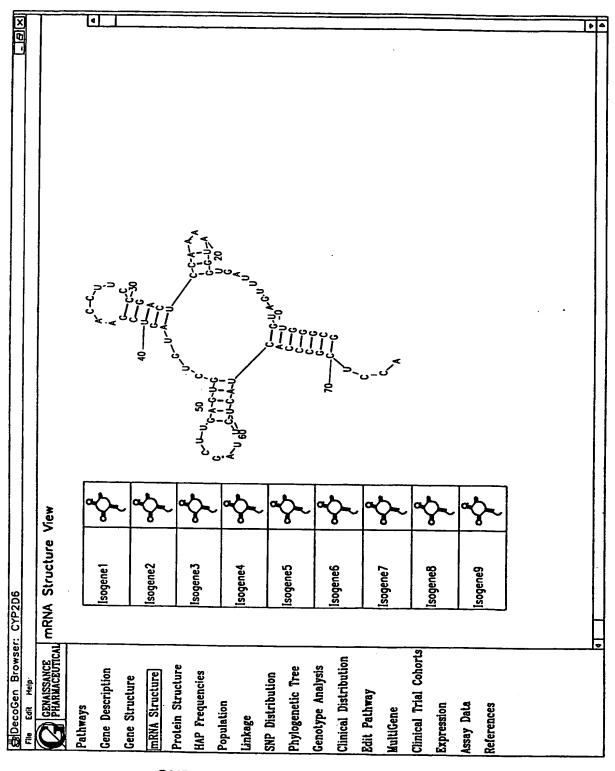
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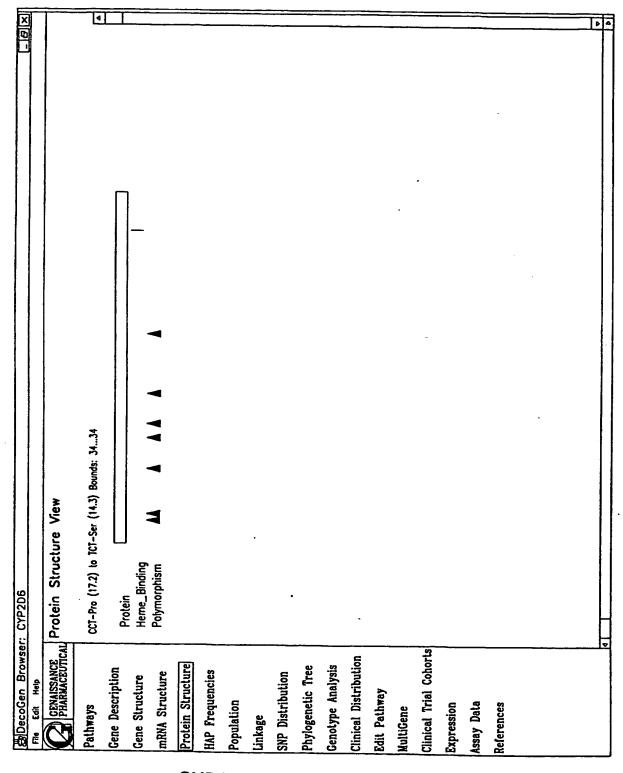
FIG.



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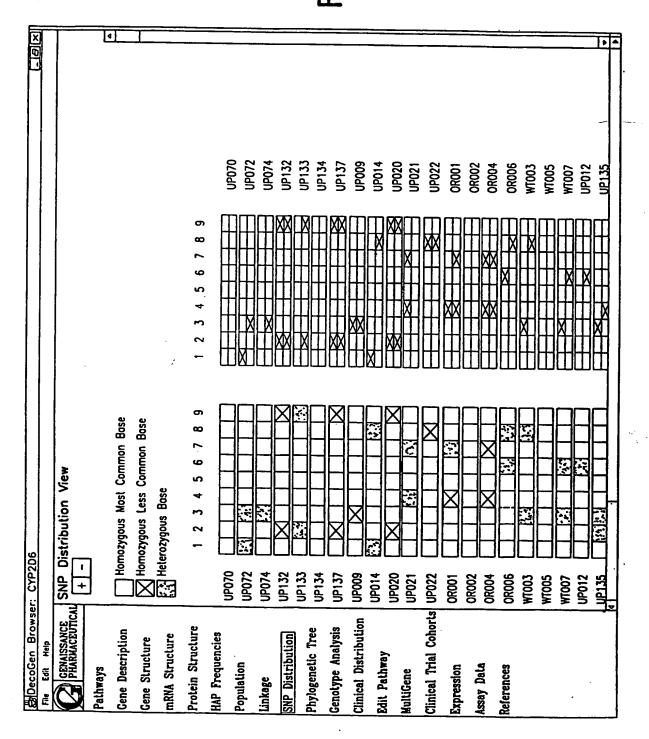


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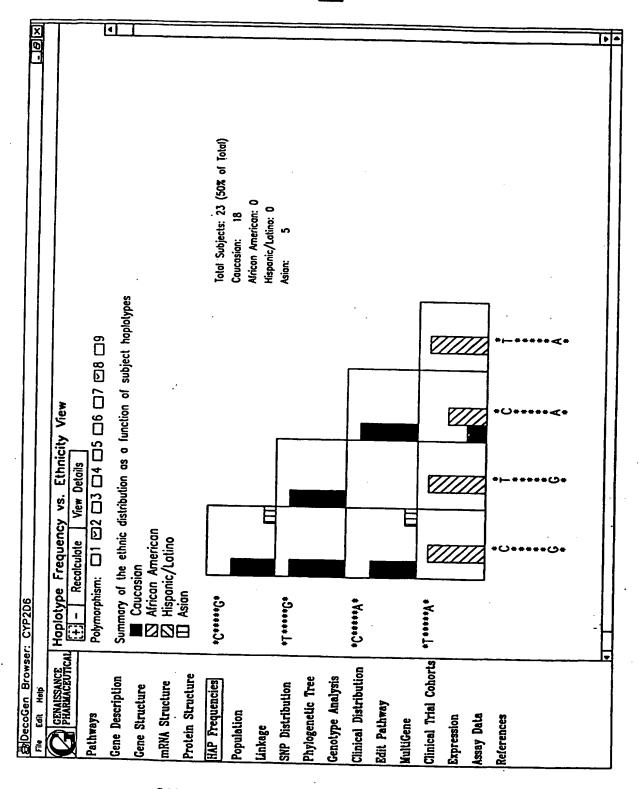
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為DecoGen Browser: CYP:	;YP206							XØ:
AISSANCE ARMACEUTICAL	Population View	>						
Pathways	PID	Ethnicity	Age	Gender	HAP 1	HAP 2	Test	4
Gene Description	UP070	CA	66	Ŀ	ссстсссс	GCCTGGCC	0.1	
Gene Structure	UP072	క	66	LL.	decereece	GCACTGGGC	0.2	
mRNA Structure	UP074	CA	66	<u>u.</u>	GCCTGGCC	GCACTGGGC	0.2	
Protein Structure	UP132	S.	66	×	crectes	GTGCTGGGT	0.3	
HAP Frequencies	UP133	క	66	M	GCCTGGC	GTGCTGGGT	0.2	
Population	UP134	క	66	Ŀ	cccrcccc	cccrcccc	0.1	
Linkage	UP137	క	66	_₹	crectes	GTGCTGGGT	0.1	
SNP Distribution	UP009	క	66	ᄔ	GCACTGGGC	GCACTGGGC	0.1	
Phylogenetic Tree	UP014	క	66	LL.	deecteece	GCGCTGGAC	0.3	
Genotype Analysis	UP020	క	66	Ŀ.	GTGCTGGGT	GTGCTGGGT	0.2	
Clinical Distribution	UP021	ర	66	<b>×</b>	ссетстс	GCGCTGGGC	0.4	
Edit Pathway	UP022	క	66	≥	GCGCTGGAC	GCGCTGGAC	0.3	
MultiGene	OR001	AS	66	×	desertesse	ссеттетес	0.2	
Clinical Trial Cohorts	OR002	Ş	66	3	GCGCTGGGC	осетесес	0.3	
Expression	0R004	ĄŞ	66	L	CACTGGGC	GCACTGGGC	0.2	
Assay Data	08006	S <del>V</del>	66	Į <b>L</b>	ССТСССС	GCGCTGGAC	0.1	
References	WT003	ర	66	la.	СССТСССС	ссеттетес	0.2	
	WT005	ర	66	3	GCGTTGGGC	GCGCTGGGC	0.2	
	WT007	క	66	×	сстстсс	ссеттетес	0.4	
	UP012	ర	66	<b>L</b> L	GCGCTAGGC	GCCTGCAC	0.1	
	UP135	ర	66	2	GCACTGGGC	GCCCTCCAC	0.2	Þ

F1G. 9

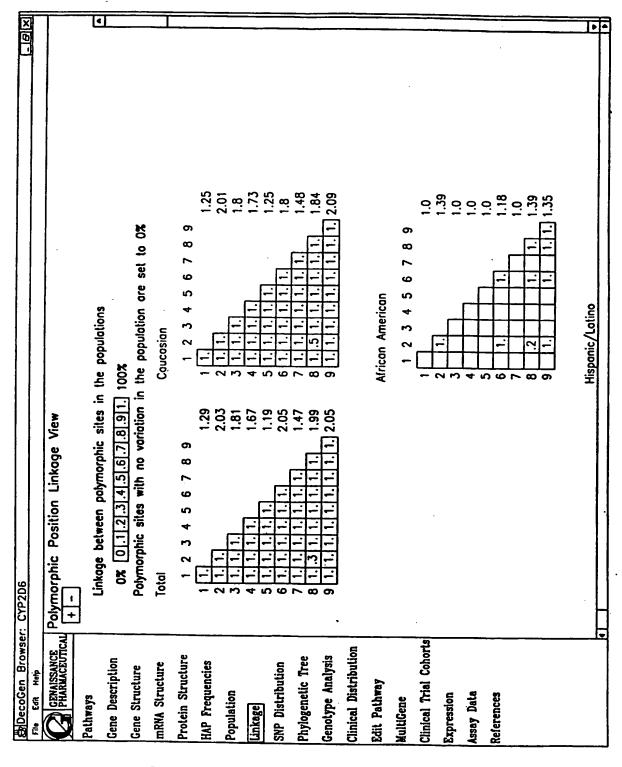


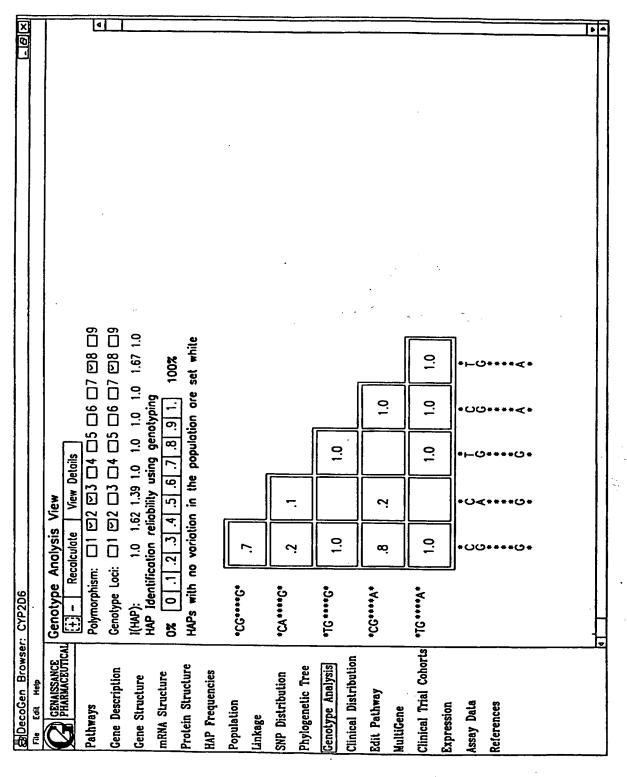
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BlDecoGen Browser: CYP2D6	: CYP206								×Θ
G GENAISSANCE PHARMACEUTICAL Pathways	Haplotype Frequency [+ -  Recalculate   [5] Polymorphism: □1 □2	doplotype Frequency vs. Ethnicity View   Commonstant   Frediculate   (View Summary)   Commonstant   Commonstant	, View □6 □7	89	6				•
Gene Description	Details of the ethnic	of the ethnic distribution as a function of subject haplotypes	tion of sut	oject hap	olotypes				
Gene Structure mRNA Structure	3 Columns are Total numb	Columns are given for each Ethnogeographic group: Total number sampled with HAP pair	geographic Idir	group:					
Protein Structure	Fraction of Fraction ex	Fraction of the ethnogeographic group with that HAP pair Fraction expected under Hordy—Weinberg equilibrium for that HAP pair	roup with teinberg equi	hot HAP	poir or that HAP pair				
HAP Frequencies	HAP 1	HAP 2	Z	XPop.	Caucasian	African American	Hispanic/Latino		-SA
Population	*C*****C*	*O*****O*	23	50%	18 56.3% 37.9%	0 0.0% 0.6%	0 0.0%		2
Linkage	*9****L*	* O * * * O *	7	\$ 5 20 20 20 20 20 20 20 20 20 20 20 20 20	2 6.3% 18.9%	0.0%	0.0%		-
	* <b>* * * * * * * *</b> * * * * * * * * * *	******	գ- ռ	% 6 6 7	4 12.3% 2.4%	0 0.0% 2.4%	0.0%	20.0	_
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Phylogenetic Tree	*V*****1*	*D*****O*		2%	0.0%	12.5%	0.0%		
Genotype Analysis	* V**** L*	* O * * * * L *	7	% 4 %	0 0.0% 0.8%	2 25.0% 18.9%	0.0%	0.0%	00
Clinical Distribution	*V*****±	* V**** L*	ח ה	8 8		3 37.5% 37.9%	0.0%		
Edit Pathway									
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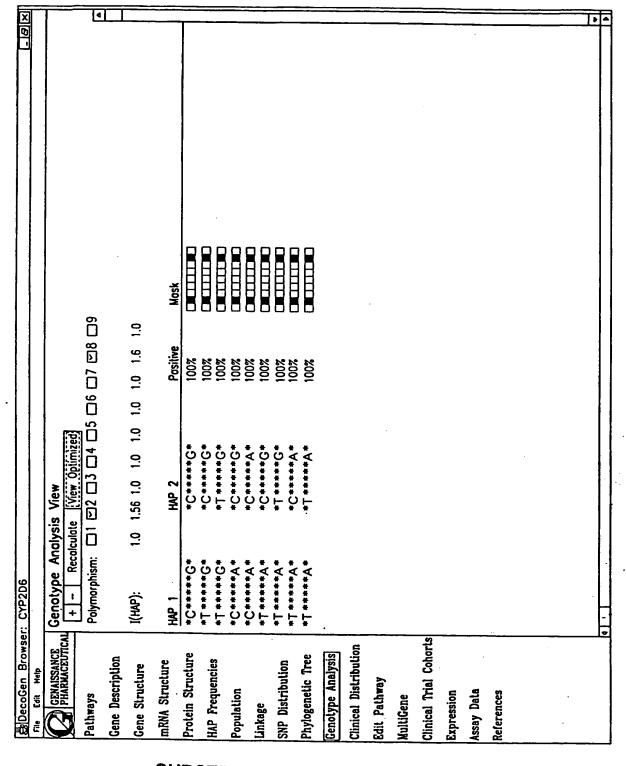


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图DecoGen Browser: CYP2D6	: CYP206				Q	
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Pathways	Polymorphism:	01 22 03 04 05 06	□7 ⊡8 □9	<u>6</u>		Ľ
Gene Description	Genotype Loci: [	01 52 03 04 05 06	□7 ⊡8 □9	6		لبك
Gene Structure		1.0 1.56 1.0 1.0 1.0 1.0	1.0 1.6 1.0			
mRNA Structure	HAP 1	HAP 2	N XPon	Positive		
Protein Structure	*D******O*	*D*****O*			22	1
HAP Frequencies	*O***** L*	**************************************	2 4%	100%	24 24	
Population	*C*****	*********		•	આ	
Linkage	*C****A*	* V***********************************	3 6%		24 24 24 24 24 24 24 24 24 24 24 24 24 2	
SNP Distribution	* V **** L*	*9*****L*	2 4%	•	· he	
Phylogenetic Tree	* Y * * * * 1 *	*V***********		1007	и и	
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Clinical Trial Cohorts						
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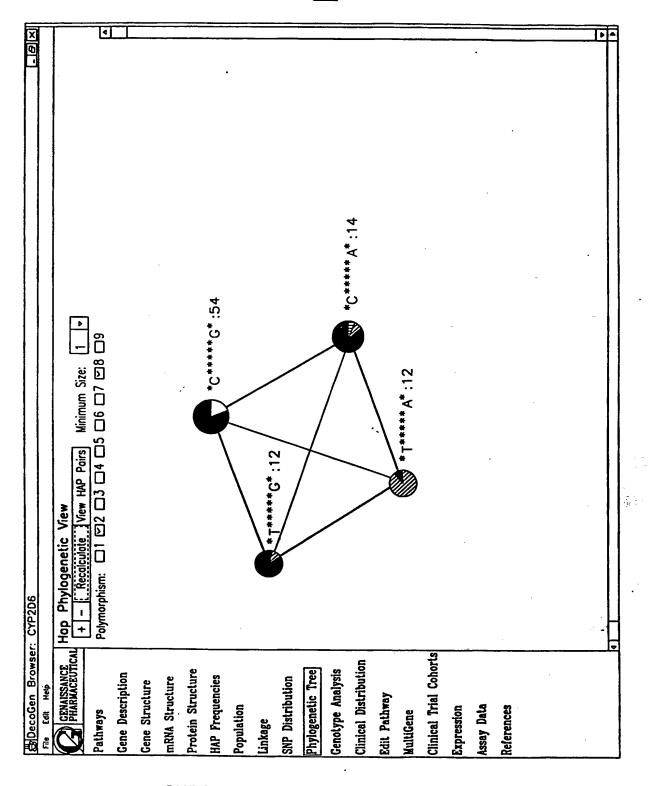
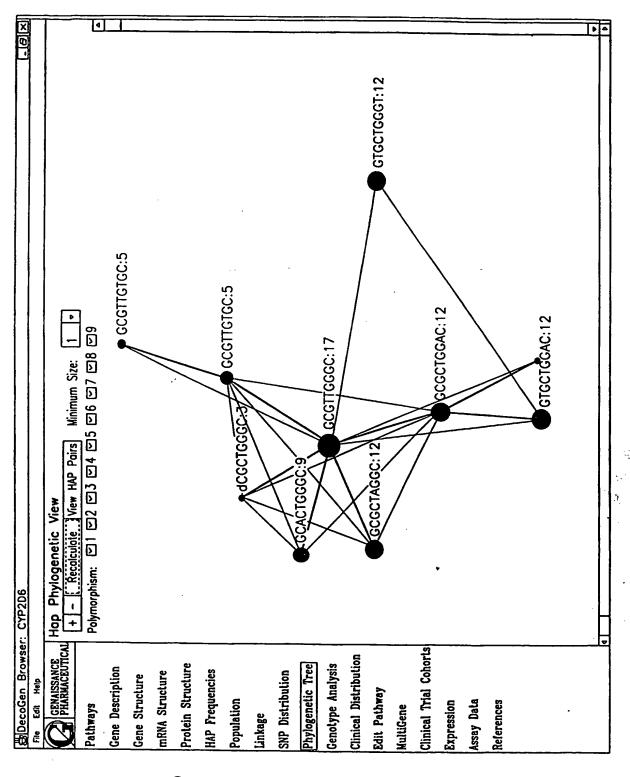
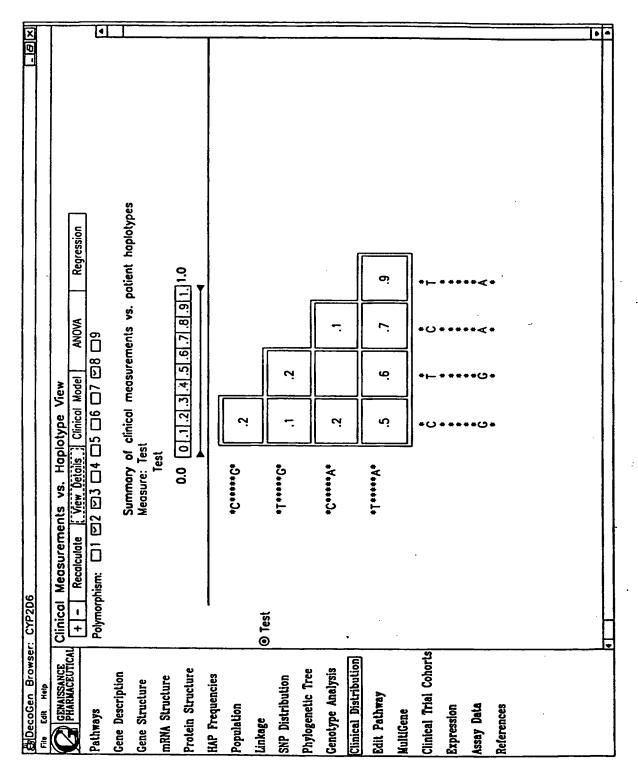
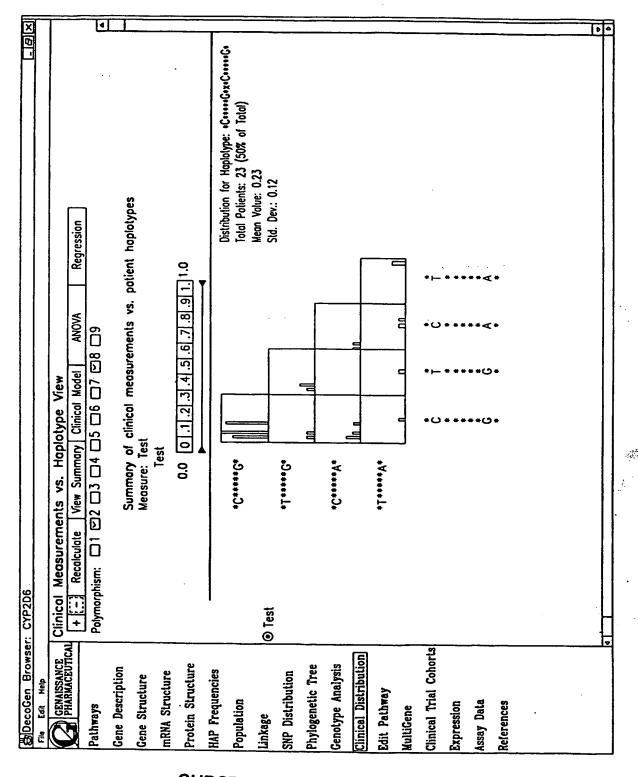


FIG. 17





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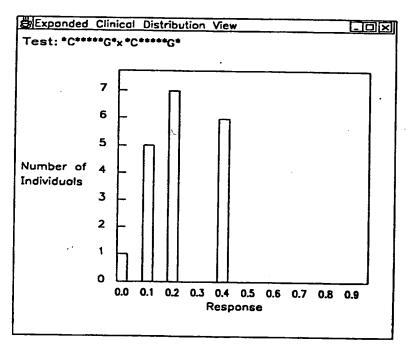


FIG. 20

Site	Slope	Intercept	Variance	T(slope)	Significance Level	
1	-0.083	0.316	0.05	-0.59	0.7223	
2	0.154	0.231	0.04	4.22	0.9999	
5	-0.08	0.326	0.05	-1.16	0.8735	
\$	-0.0080	0.313	0.06	-0.14	0.5572	
<b>i</b>	0.145	0.305	0.05	0.86	0.804	
5	-0.08	0.332	0.05	-1.24	0.8902	
,	0.0070	0.31	0.06	80.0	0.5303	
3	0.158	0.222	0.04	4.34	1.0	
}	-0.043	0.322	0.05	-0.76	0.7752	
		,				

FIG. 21

BDecoGen Browser: CY	: CYP2D6	5							×  8  -
File Edit Help									
GENAISSANCE PHARMACEUTICAL	Cinic	Measurem							
Pathways		Polymorphism: 1 2 13 4 5 6 7 8 9	Ical Model ANUVA	Кеди	Kegression				
Gene Description		Summary of clinic	Summary of clinical measurements vs. potient hoplotypes	potient h	aplotype	Ş.			
Gene Structure		Meosure: Test Test							
Protein Structure		0.0	.2[.3 .4[.5].6 .7].8	9 1.0					
HAP Frequencies	ŀ								
Population	⊙ Test	HAP 1	Hop 2	Z	XPop.	Mean	Siddev X**2	X2	0(x • 2  K - 3)
Linkage		**************	*5******	23	20%	0.24		9.17	_
SNP Distribution		******	**************************************	<b>~</b> 4	4 % % %	0.15	0.07	0.0	1.0 (-3)
Phylogenetic Tree		*V*****O*	********	. ი	10%	0.22		0.8	1.0 (-2)
Genotyne Analysis		*C****A*	*C*****	m ·	%9	0.13		0.0	_
ciclinia od formo		* * * * * * * * * * * * * * * * * * * *	*O************************************	<b>-</b> - (	2%	o.5		0.0	_
Clinical Distribution		******	************************	7 ٢	4 G % %	رن دري	o. c	) ) )	(S-) (S-) (S-)
Edit Pathway		*V****1*	*V*****L*	ייי ני	88	0.93		0.0	_
MultiGene									
Clinical Trial Cohorts									
Expression									
Assay Data	<b>⊙</b> Test								
References									
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+ -   Re	calculate				
Polymorphism		J3 □4 C	⊃5 <b>□</b> 6 □	コ7 図8 🗆 9	_
Source of Va	riation DF	Mean Squar	res F-ratio		1
Between Grou	•	0.26	19.65	•	_
Within Groups	37	0.01	13.00		
Critical F-Dis	tribution Value 90	X: 1.88		•	- [
	tribution Value 95				
Critical F-Dis	tribution Value 99	<b>%</b> : 3.16			Ì
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NADDITIONAL PA				CE JEWNI	
	tween-group varia				
Significant be	tween-group varia	tion at the	95% confide	nce level	
Significant be		tion at the	95% confide	nce level	
Significant be	tween-group varia	tion at the	95% confide	nce level nce level	
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Significant be Significant be HAP 1	tween-group varia  HAP 2  *C*****G*	tion at the tion at the N 23	95% confide 99% confide Average 0.23	nce level nce level Std. Dev. 0.12	
Significant be Significant be 'HAP 1 *C*****G* *C*****G*	tween-group varia  HAP 2  *C*****G*  *T*****G*	tion at the tion at the N 23 2	95% confide 99% confide Average 0.23 0.15	Std. Dev.  0.12 0.07	_
Significant be Significant be 'HAP 1  *C*****G*  *C*****G*	tween-group varia  HAP 2  *C*****G*  *C*****A*	tion at the tion at the N 23 2 5	95% confide 99% confide Average 0.23 0.15 0.22	Std. Dev.  0.12 0.07 0.13	_
Significant be Significant be  'HAP 1  •C*****G*  •C*****G*	tween-group varia  HAP 2  *C*****G*  *C*****A*  *T*****G*	tion at the tion at the N 23 2 5 4	95% confide 99% confide Average 0.23 0.15 0.22 0.2	Std. Dev.  0.12 0.07 0.13 0.08	
Significant be Significant be  'HAP 1  • C******G* • C*****G* • C*****G*	tween-group varia  HAP 2  *C*****G*  *C*****G*  *C******G*  *T*****G*  *T******G*	tion at the tion at the N 23 2 5 4 2	95% confide 99% confide Average 0.23 0.15 0.22 0.2 0.55	Std. Dev.  0.12 0.07 0.13 0.08 0.07	_
Significant be Significant be  'HAP 1  • C******G* • C******G* • T*****G* • T*****G* • C*****A*	tween-group varia  HAP 2  *C*****G*  *T*****G*  *T*****G*  *T*****A*	tion at the tion at the N 23 2 5 4 2 3 3	95% confide 99% confide Average 0.23 0.15 0.22 0.2 0.55 0.13	Std. Dev.  0.12 0.07 0.13 0.08 0.07 0.15	
Significant be Significant be Significant be  'HAP 1  • C*******G* • C******G* • C******A* • C*****A*	HAP 2  *C*****G*  *T*****G*  *T*****G*  *T*****G*  *T*****G*  *T*****G*  *T*****G*  *T*****A*  *T*****A*	tion at the tion at the N 23 2 5 4 2 3 3 3	95% confide 99% confide Average 0.23 0.15 0.22 0.2 0.55 0.13 0.6	Std. Dev.  0.12 0.07 0.13 0.08 0.07 0.15 0.09	

FIG. 23

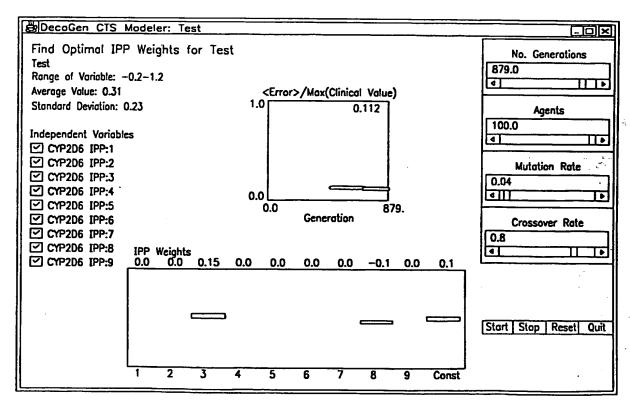
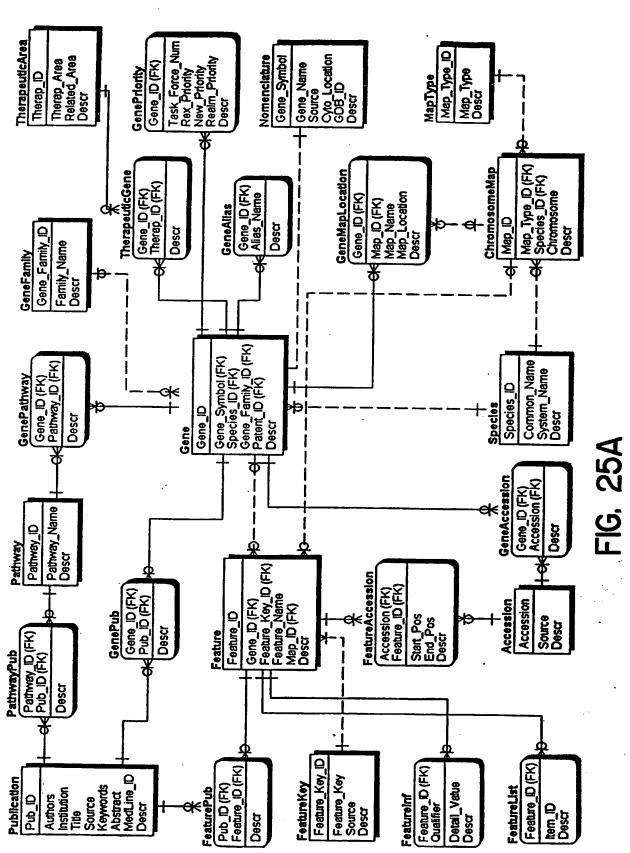
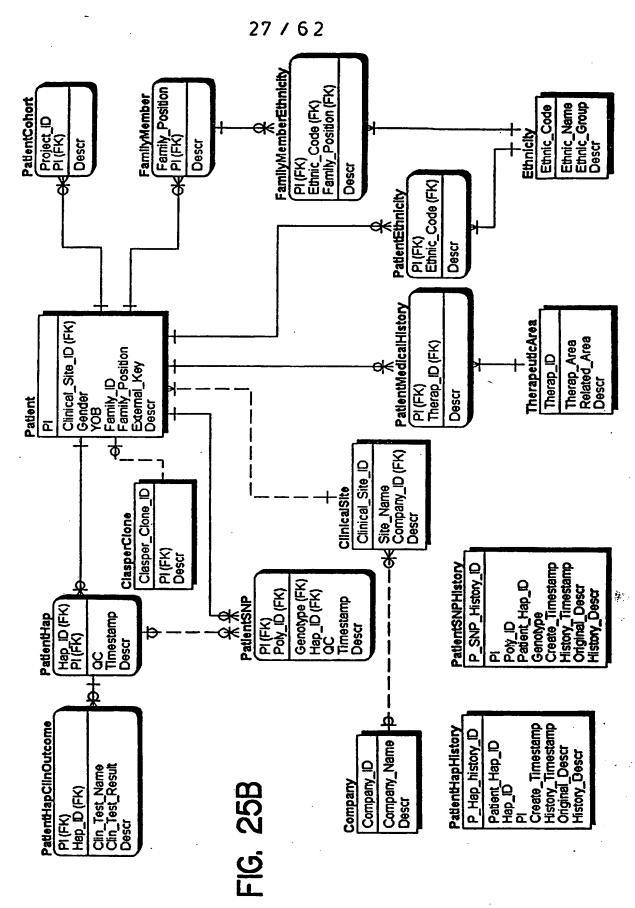


FIG. 24
SUBSTITUTE SHEET (RULE 26)

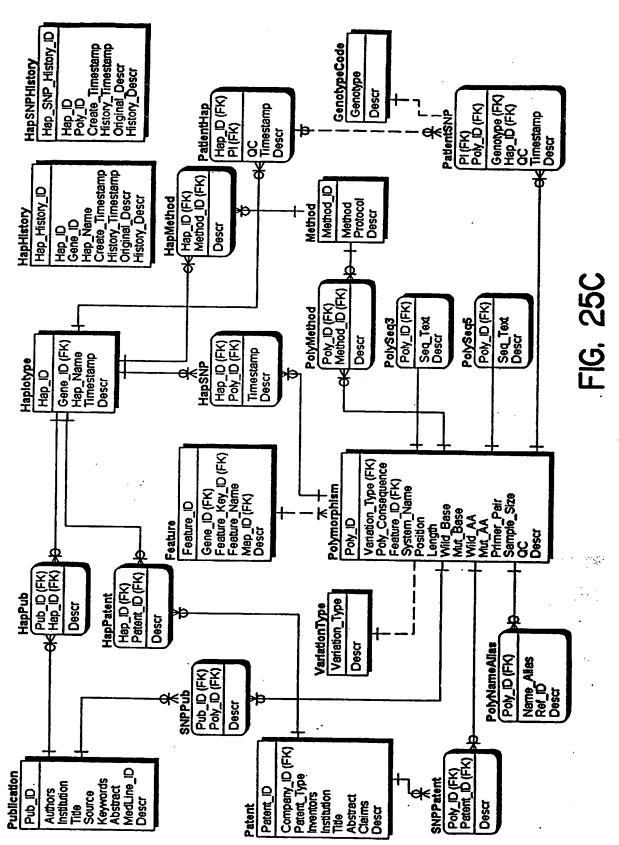


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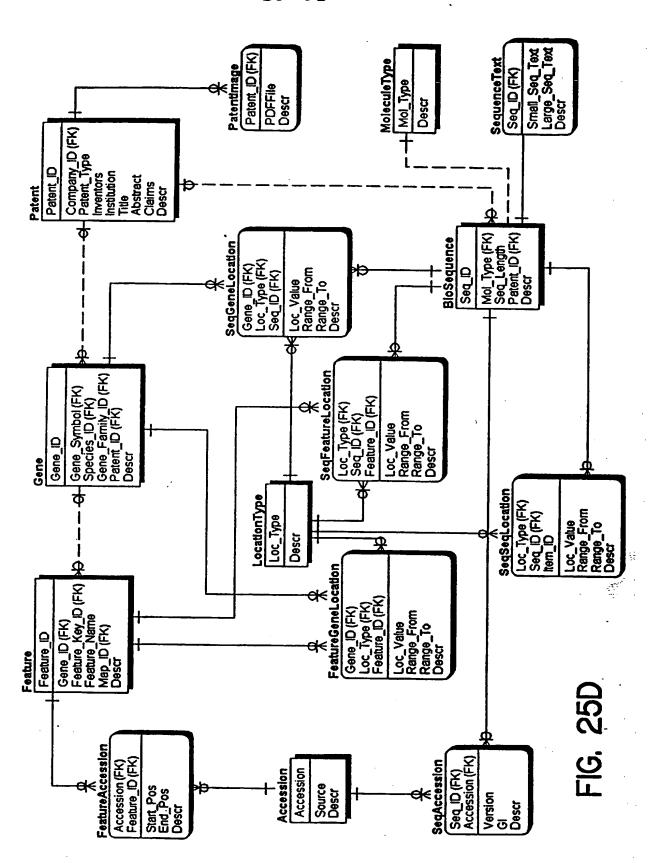
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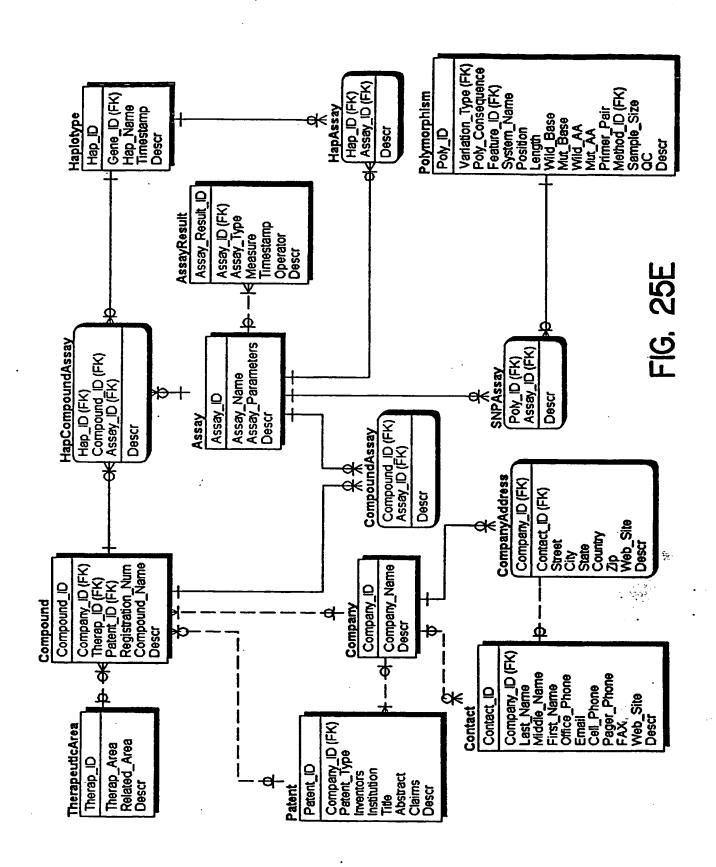


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## Legend of Figures:



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Rectangle Boxes: Tables in the database.



Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 10: |----- Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 12: --- Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.
- 14: +-- Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

## FIG. 25F

FIG. 26

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Extracellular OADBR2 High phyogenetic Extracellular OADBR2 High phyogenetic Interpretations High physical Inte | Extracellular   CADBR2   Extracellular   CADBR2   Extracellular   CADBR2   Extracellular   CADBR2   Extracellular   CADBR2   Extracellular   CADBR2   CADBR3   CADB   | Linkage  Lin | Linkage Linkag | Linkage Linkag | Extracellular OADBR2   | Linkage  Lin | Linkage Linkag | Linkage Linkag | Linkage  Lin | Linkage  Lin | Linkage Linkag | Linkage Linkag | Linkage ians Li | Extracellular  | Linkage Linkag | Extracellular  | High Linkage   Trial Data ariables orrelations ariables ariable | Trial Data ariables orrelations orrelations Intracellular OADBR2 orrelations Intracellular OADBR2 Intracellular OADBR2 Intracellular OADE68 OPDE68 OcalM1  | Trial Data ariables orrelations ariables Intracellular OADBR2 ariables orrelations Intracellular OADBR2 Intracellular OADBR2 Intracellular OPDE6B OSease   
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  |  |  | — EHAPpair   | -EHAPPoir  | — The Habbair  
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   | Fig. Politen Lobie   | Folient toble  Fig HAPTyping  Fig HAPPoir  | Polient toble  Haryping  HAPPoir   | E Potient toble  E HAPTiping  HAPPair  | Potient toble  HaryTyping  HAPPair  
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FIG. 27

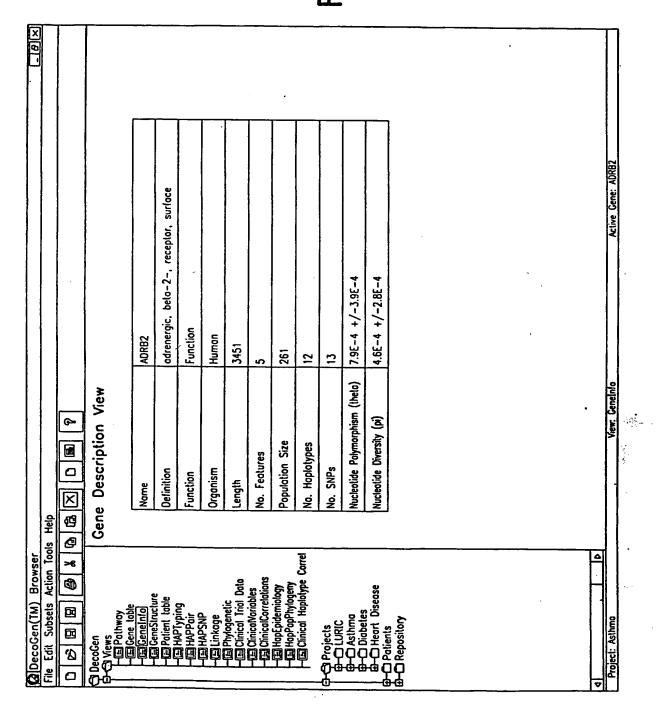
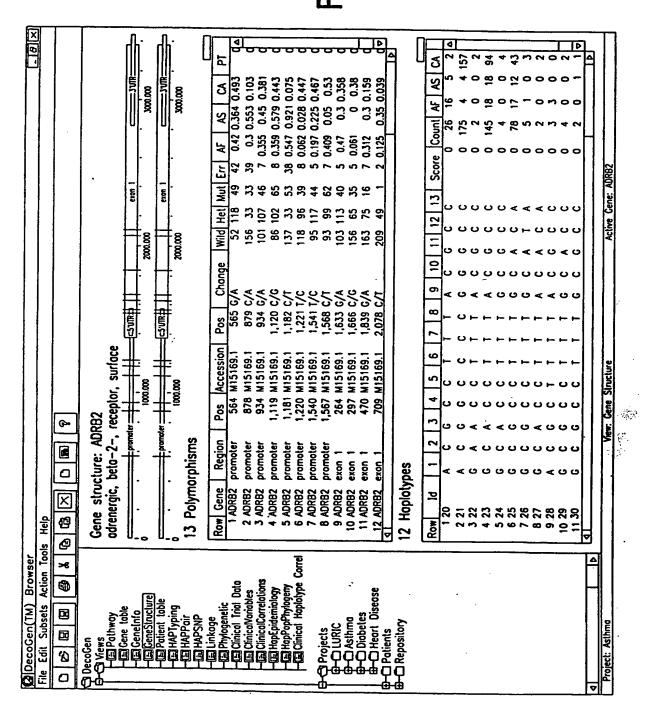
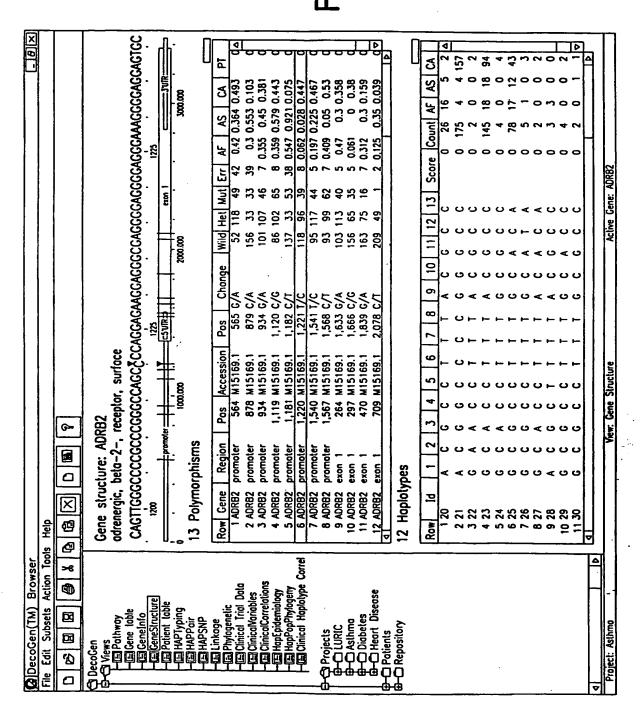


FIG. 28A



SUBSTITUTE SHEET (RULE 26)

FIG. 28B



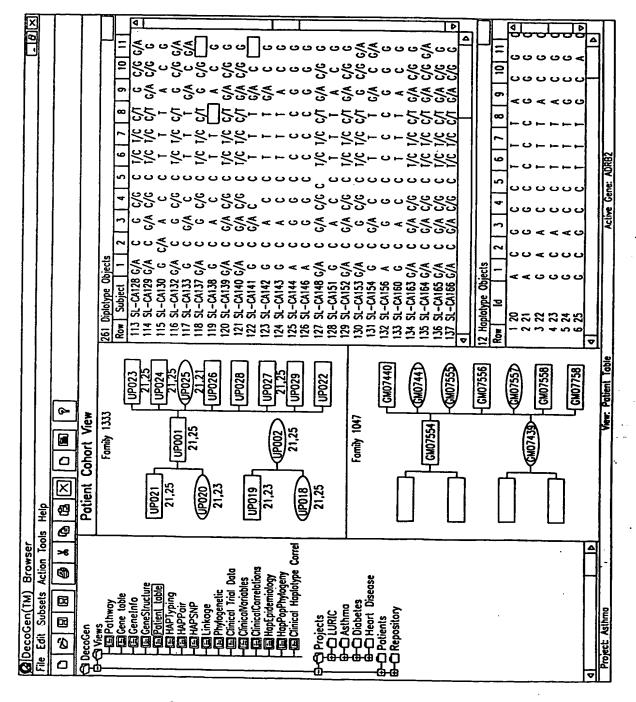
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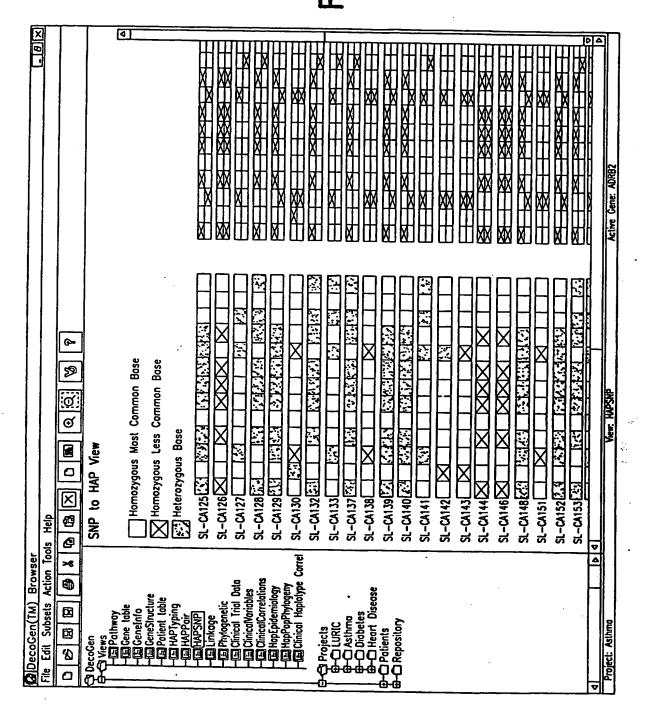


SUBSTITUTE SHEET (RULE 26)

<u>등</u> 29

Clinical Trial Data   Parish   Parish   Parish   Parish   Potentikessurement Objects   Parish   Patient   Severit Skin les Prc. Parish   Patient   Patient   Severit Skin les Prc. Parish   Patient   Pa	(A) DecoGen(TM) Browser											N N
Clinical Froid   Clinical Froid   Data   Parente   Clinical Froid   Data   Parente   Clinical Froid   Data   Parente   Clinical Froid   Data   Parente   Parente   Clinical Froid   Data   Parente   Parente	Edit Subsets Action											=1
Clinical Trial Dota   Clinical Froil Dota   Clinical Froil Dota   Clinical Froil F		<b>₩</b>				ļ						
Polithwey   Comparison   Comp	G Decogen	Clinical Trial	Data									
Constitution   Cons	₽-	182 PatientMeasure	nent Objects									L
Control   Cont	Cene toble		Severity	Skin Tes		2		,	$\overline{}$	臣	臣	_
Care Structure   25SA4134   2.0   1.0   2.0   54.0   0.96   34.0   48.0   0.45   12.0   1	GeneInfo	1 SL-A4131	2.0	1.0	1.88	58.0	1.28	52.0	68.0	8.	49.0	-
Comparing the black   35,2-A136   0.0   0.2   0.5	-E GeneStructure	2 SL-A4134	2.0	1.0	2.01	54.0	96.0	34.0	48.0	0.45	12.0	2.2
Light Hyperical Control Cont	Potient toble	3 SL-A4136	0.0	0.0	2.56	89.0	2.22	93.0	87.0	3.2	91.0	2.5
March Part   SSL-AMISS   Z.O   1.0   1.77   4.00   0.98   27.0   55.0   0.66   15.0   22.2     March Part   SSL-AMISS   Z.O   1.0   4.28   96.0   1.71   95.0   63.0   1.48   3.00   4.4     March Part   SSL-AMISS   Z.O   1.0   3.44   91.0   1.97   66.0   57.0   6.35   57.0   5.5     March Editined Incid Della   SSL-AMISS   Z.O   0.0   3.44   91.0   1.97   66.0   57.0   0.35   1.10   2.5     March Editined Incid Della   SSL-AMISS   Z.O   0.0   0.0   0.0   0.0   0.0   0.0   0.0     March Editined Incid Della   SSL-AMISS   Z.O   0.0   0	HE HAPTyping	4 SL-A4150	2.0	1.0	1.4	50.0	9.0	27.0	43.0	0.22	7.0	1.5
Size-Arise   Size-Arise   Low   Lo	- HAPPoir	5 SL-A4155	2.0	1.0	1.77	40.0	0.98	27.0	55.0	0.61	16.0	2.2
Second Hopotype Correlations	THE HAPSNE	6 SL-A4159	2.0	0.1	2.89	0.99	1.71	51.0	59.0	6.0	20.0	4.4
Size   March   Size   March   Size	7 SL-AA195	1.0	1.0	4.28	96.0	2.7	79.0	63.0	1.48	33.0	5.2	
SIS-AA27   2.0   0.0   1.93   54.0   0.96   37.0   49.0   0.35   11.0   2.5	Tiest Trision Trision	8 SL-AA211	1.0	1.0	3.44	91.0	1.97	0.99	57.0	1.39	32.0	5.5
International   Internationa	Carlo Carlo	9 St AA227	2.0	0.0	1.93	54.0	96.0	37.0	49.0	0.35	0.1	2.5
1151—AA270   NP   NP   NP   NP   NP   NP   NP   N	TEL CHILICON OF TORREST	2	1.0	1.0	3.0	0.96	10.7	70.0	57.0	0.99	25.0	3.8
12 SiCA105	Tell Honfordemiology	=	ď	ďΝ	dΝ	dN	٩N	<u>₽</u>	₽	₽	₽	g⊵
13 SL-CA101   1.0   1.0   2.17   85.0   1.92   64.0   71.0   1.33   38.0   3.2     14 SL-CA103   2.0   1.0   2.56   59.0   2.16   45.0   61.0   1.13   18.0   4.1     15 SL-CA104   2.0   0.0   1.99   62.0   1.11   46.0   57.0   0.55   24.0   2.34     15 SL-CA105   2.0   0.0   1.99   62.0   1.11   46.0   57.0   0.55   24.0   2.34     15 SL-CA106   0.0   1.0   3.46   82.0   2.59   83.0   37.0   0.55   24.0   2.38     16 SL-CA109   1.0   1.0   2.63   93.0   1.7   7.0   64.5   0.89   2.50   2.8     17 SL-CA110   0.0   1.0   2.63   93.0   1.7   7.0   64.5   0.89   2.50   2.8     18 SL-CA110   0.0   1.0   2.64   83.0   1.7   7.0   64.5   0.89   2.50   3.3     19 SL-CA110   0.0   1.0   2.44   83.0   1.7   7.0   64.5   0.89   2.50   3.3     22 SL-CA111   1.0   1.0   2.44   83.0   1.31   79.0   78.0   1.17   43.0   2.4     23 SL-CA112   1.0   1.0   2.44   83.0   1.37   71.0   83.0   1.37   43.0   2.4     24 SL-CA12   1.0   1.0   2.44   83.0   1.37   71.0   83.0   1.37   43.0   1.4     25 SL-CA112   1.0   1.0   2.44   83.0   1.37   71.0   83.0   1.37   43.0   1.4     28 SL-CA12   1.0   1.0   2.44   83.0   1.37   83.0   1.4   83.0   1.4     28 SL-CA12   2.0   1.0   4.24   106.0   2.7   83.0   63.0   0.9   2.5   62.0   6.0     29 SL-CA12   2.0   1.0   4.24   106.0   2.7   83.0   63.0   0.41   1.2   2.5     29 SL-CA12   2.0   1.0   1.3   80.0   1.3   70.0   62.0   0.9   2.5   62.0   6.0     29 SL-CA12   2.0   1.0   1.3   42.0   0.81   37.0   68.0   0.41   1.0   2.5     34 SL-CA12   2.0   0.0   1.7   64.0   1.3   1.3   1.3   1.4   1.0   1.3   1.3   1.4     1	Handonday	12	NP	NP	dΝ	ďΝ	ď	dN	ջ	₽	<u>S</u>	g Z
14 Si = CA103   2.0   1.0   3.56   59.0   2.16   46.0   61.0   1.13   18.0   4.1     15 Si = CA104   2.0   0.0   2.76   57.0   146   39.0   53.0   0.59   16.0   3.4     15 Si = CA106   0.0   1.0   3.82   13.0   2.59   83.0   57.0   0.55   24.0   2.3     16 Si = CA106   0.0   1.0   3.82   13.0   2.59   83.0   37.0   0.55   24.0   2.3     17 Si = CA107   0.0   1.0   3.82   13.0   2.59   83.0   3.9   3.9     18 Si = CA108   NP   NP   NP   NP   NP   NP   NP   N	(E) Clinical Hoplotype Correl	13	1.0		2.17	85.0	1.92	64.0	71.0	1.33	38.0	3.2
⊕ Projects         15 SL-CA104         2.0         0.0         2.76         57.0         1.46         19.0         53.0         0.55         24.0         2.3           ⊕ Dunklic         16 SL-CA105         2.0         0.0         1.99         62.0         1.11         46.0         57.0         0.55         24.0         2.3           ⊕ Dubbetes         18 SL-CA107         0.0         1.0         3.46         8.20         2.69         83.0         57.0         0.25         24.0         2.3           ⊕ Diobetes         18 SL-CA107         0.0         1.0         3.82         1.3         1.7         4.60         57.0         0.25         24.0         2.3           ⊕ Diobetes         18 SL-CA107         0.0         1.0         3.82         1.7         7.0         1.77         4.60         3.9           Debtients         2.0 SL-CA119         NP		14			3.56	59.0	2.16	46.0	61.0	1.13	18.0	1.
⊕-CiuRIC         16 SI-CA105         2.0         0.0         1.9         6.2.0         1.11         46.0         57.0         0.55         24.0         2.3           ⊕-ChiuRIC         17 SI-CA106         0.0         1.0         3.46         82.0         2.69         83.0         57.0         2.28         51.0         4.4           ⊕-Diobetes         18 SI-CA108         NP         N	[마스] Projects	15 SL -CA104			2.76	57.0	1.46	39.0	53.0	0.59	16.0	3.4
## Chopetes  17 SI.—CA106 0.0 1.0 3.46 82.0 2.69 83.0 57.0 2.28 51.0 4.4  □ Chobetes  18 SI.—CA107 0.0 1.0 3.82 113.0 2.59 83.0 78.0 1.7 46.0 39.9  □ Cheart Discose  19 SI.—CA109 1.0 1.0 2.63 93.0 17.0 1.7 46.0 39.9  □ Cheart Discose  20 SI.—CA109 1.0 1.0 4.56 114.0 1.8 101.0 70.0 2.24 51.0 4.5  22 SI.—CA11 2.0 1.0 3.08 69.0 2.01 58.0 65.0 1.7 43.0 3.0  23 SI.—CA11 1.0 0.0 2.83 84.0 2.18 77.0 77.0 1.77 43.0 3.0  24 SI.—CA11 1.0 0.0 2.84 83.0 1.37 77.0 1.77 43.0 3.0  25 SI.—CA11 1.0 1.0 1.53 76.0 1.27 69.0 1.27 49.0 1.6  27 SI.—CA12 1.0 1.0 4.24 106.0 2.71 83.0 64.0 1.8 10.0 1.27 49.0 1.6  28 SI.—CA12 0.0 1.0 4.24 106.0 2.71 83.0 62.0 0.95 26.0 3.6  29 SI.—CA12 0.0 1.0 4.24 106.0 2.71 83.0 62.0 0.95 26.0 3.6  30 SI.—CA12 0.0 1.0 5.76 105.0 4.35 103.0 75.5 3.52 62.0 6.0  31 SI.—CA12 2.0 1.0 1.82 66.0 0.97 70.0 62.0 0.95 26.0 1.3  31 SI.—CA12 2.0 1.0 1.8 66.0 0.97 40.0 50.0 0.41 11.0 2.5  32 SI.—CA12 1.0 1.0 5.76 105.0 4.35 103.0 75.5 3.52 62.0 6.0  34 SI.—CA12 1.0 1.0 5.76 105.0 1.3 43.0 53.0 0.41 11.0 2.5  34 SI.—CA12 1.0 1.0 1.82 66.0 0.97 75.0 0.95 18.0 1.8  34 SI.—CA12 1.0 1.0 1.9 66.0 0.97 40.0 50.0 0.41 11.0 2.5  34 SI.—CA12 1.0 1.0 1.0 5.76 105.0 1.3 43.0 53.0 0.41 11.0 2.5  34 SI.—CA12 1.0 1.0 1.0 5.76 105.0 0.81 0.81 0.41 11.0 2.5  34 SI.—CA12 2.0 0.0 1.74 64.0 1.17 52.0 0.81 0.81 0.41 11.0 2.5  34 SI.—CA12 1.0 1.0 1.0 1.82 66.0 0.97 75.0 0.95 1.81 0.81 0.81 0.41 11.0 2.5  34 SI.—CA12 1.0 1.0 1.0 1.82 66.0 0.91 3.0 0.41 11.0 2.5  34 SI.—CA12 1.0 1.0 1.3 68.0 0.41 11.0 2.5 18.0 1.81 0.81 0.41 1.10 2.5  35 SI.—CA12 1.0 1.0 1.3 68.0 0.91 1.3 1.3 43.0 68.0 0.41 11.0 2.5 18.0 1.81 0.81 0.41 0.41 0.41 0.41 0.41 0.41 0.41 0.4	— <del>p</del> -D turic	16 SL-CA105			1.99	62.0	1.11	46.0	57.0	0.55	24.0	2.3
#☐ Diobetes 18 SL—CA107 0.0 1.0 3.82 113.0 2.59 83.0 78.0 1.7 46.0 3.9   #☐ Diobetes 19 SL—CA108 NP	E-C) Asthmo	17 SL-CA106			3.46	82.0	2.69	83.0	57.0	2.28	51.0	4.4
To Separate Disease 19 SL-CA108 NP	- Diobetes	18 SL-CA107	0.0		3.82	113.0	2.59	83.0	78.0	1.7	46.0	3.9
Colored State		19 SL-CA108	ΔN		٩	ΝĐ	ΝP	dN.	Νb	dN	ΝP	œ.
Color		20 StCA109	1.0		2.63	93.0	1.7	7.0	64.5	0.89	25.0	2.8
22 SL-CA111 2.0 1.0 3.08 69.0 2.01 58.0 65.0 1.12 32.0 3.3 2.1 5.2 SL-CA114 1.0 0.0 2.83 84.0 2.18 77.0 77.0 1.77 43.0 3.0 3.0 2.4 2.4 83.0 1.91 79.0 77.0 1.77 43.0 3.0 2.4 2.4 SL-CA116 1.0 1.0 2.4 83.0 1.91 79.0 78.0 1.8 49.0 2.4 2.4 2.4 SL-CA118 1.0 1.0 3.81 90.0 2.25 67.0 59.0 1.04 22.0 4.1 2.5 SL-CA118 1.0 1.0 1.53 76.0 1.27 71.0 83.0 1.27 49.0 1.6 1.6 27 SL-CA19 NP			0.0		4.56	114.0	3.18	101.0	70.0	12.24	51.0	4.5
23 SL-CA114   1.0   0.0   2.83   84.0   2.18   77.0   77.0   1.77   43.0   3.0   2.4   SL-CA116   1.0   1.0   2.4   83.0   1.91   79.0   78.0   1.8   49.0   2.4   2.4   2.5   2.4   2.5   2.5   2.5   2.4   2.5					3.08	69.0	2.01	58.0	65.0	1.12	32.0	3.3
24 SL-CA116 1.0 1.0 2.4 83.0 1.91 79.0 78.0 1.8 49.0 2.4 2.5		23 SL-CA114			2.83	84.0	2.18	77.0	77.0	11.77	43.0	3.0
25 SL-CA117 1.0 1.0 3.81 90.0 2.25 67.0 59.0 1.04 22.0 4.1   26 SL-CA118 1.0 1.0 1.53 76.0 1.27 71.0 83.0 1.27 49.0 1.6   27 SL-CA119 NP		24 SL-CA116	1.0		2.44	83.0	1.91	79.0	78.0	1.8	49.0	2.4
26   SL-CA118   1.0   1.0   1.53   76.0   1.27   71.0   83.0   1.27   49.0   1.61		25 SL-CA117	1.0		3.81	90.0	2.25	67.0	59.0	1.04	22.0	4.1
27   SL-CA19   NP   NP   NP   NP   NP   NP   NP   N		26 St CA118	1.0		1.53	76.0	1.27	71.0	83.0	1.27	49.0	9.
28   SL-CA120   0.0   1.0   4.24   106.0   2.71   83.0   64.0   1.61   33.0   4.4,     29   SL-CA121   1.0   0.0   3.05   88.0   1.9   70.0   62.0   0.95   26.0   3.6,     30   SL-CA122   0.0   1.0   5.76   105.0   4.35   103.0   75.5   3.52   62.0   6.0,     31   SL-CA123   2.0   1.0   1.82   66.0   0.92   40.0   50.0   0.41   12.0   2.5,     32   SL-CA124   2.0   0.0   2.45   59.0   1.3   43.0   53.0   0.41   11.0   2.5,     33   SL-CA125   2.0   1.0   1.19   42.0   0.81   37.0   68.0   0.47   22.0   1.3,     34   SL-CA126   2.0   0.0   1.74   64.0   1.17   52.0   67.0   0.55   18.0   1.8,     35   SL-CA127   1.0   1.0   1.07   68.7   1.63   73.0   81.0   1.49   66.6   7.6     44		27 St -CA119	d.		٩	ď	NP.	dN	dN	JN	dN	₫.
29 SL-CA121   1.0   0.0   3.05   88.0   1.9   70.0   62.0   0.95   26.0   3.61     30 SL-CA122   0.0   1.0   5.76   105.0   4.35   103.0   75.5   3.52   62.0   6.03     31 SL-CA123   2.0   1.0   1.82   66.0   0.92   40.0   50.0   0.41   12.0   2.51     32 SL-CA124   2.0   0.0   2.45   59.0   1.3   43.0   53.0   0.41   11.0   2.51     33 SL-CA125   2.0   1.0   1.19   42.0   0.81   37.0   68.0   0.47   22.0   1.3     34 SL-CA126   2.0   0.0   1.74   64.0   1.17   52.0   67.0   0.55   18.0   1.81     35 SL-CA127   1.0   1.07   68.7   16.3   73.0   81.0   1.49   66.6   7.6     4		28 SL-CA120	$\exists$		4.24	106.0	2.71	83.0	64.0	1.61	33.0	4.4
30 StCA122   0.0   1.0   5.76   105.0   4.35   103.0   75.5   3.52   62.0   6.07     31 StCA123   2.0   1.0   1.82   66.0   0.92   40.0   50.0   0.41   12.0   2.51     32 StCA124   2.0   0.0   2.45   59.0   1.3   43.0   53.0   0.41   11.0   2.51     33 StCA125   2.0   1.0   1.19   42.0   0.81   37.0   68.0   0.47   22.0   1.3     34 StCA126   2.0   0.0   1.74   64.0   1.17   52.0   67.0   0.55   18.0   1.81     35 StCA127   1.0   1.07   68.7   1.53   73.0   83.0   1.49   66.6   7.6     4 StCA127   1.0   1.07   68.7   1.53   73.0   73.0   73.0   73.0     5 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     5 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     6 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     7 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     7 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     8 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     9 StCA127   1.0   1.07   68.7   1.63   73.0   73.0   73.0     9 StCA127   1.0   1.07   68.7   1.63   73.0   73.0     9 StCA127   1.0   1.07   68.7   1.63   73.0     9 StCA127   1.0   1.07   68.0   1.08   73.0     9 StCA127   1.0   1.07   68.0   1.07   1.08   73.0     9 StCA127   1.0   1.07   1.07   1.08   73.0     9 StCA127   1.0   1.07   1.07   1.08		29 St -CA121			3.05	88.0	1.9	70.0	62.0	0.95	26.0	3.6
31 SL-CA123   2.0   1.0   1.82   66.0   0.92   40.0   50.0   0.41   12.0   2.53		30 SL-CA122	0.0		5.76	105.0	4.35	103.0	75.5	3.52	62.0	6.0
32 SL—CA124   2.0   0.0   2.45   59.0   1.3   43.0   53.0   0.41   11.0   2.51   33.0   33.		31 SL-CA123			1.82	0.99	0.92	40.0	50.0	0.41	12.0	2.5
33 SL - CA125   2.0   1.0   1.19   42.0   0.81   37.0   68.0   0.47   22.0   1.3   34 SL - CA126   2.0   0.0   1.74   64.0   1.17   52.0   67.0   0.55   18.0   1.8   35 SL - CA127   1.0   1.07   68.7   1.63   73.0   83.0   1.49   66.6   7		32 SL-CA124			2.45	29.0	1.3 E.1	43.0	53.0	0.41	0.1	2.5
34 SL-CA126   2.0   0.0   1.74   64.0   1.17   52.0   67.0   0.55   18.0   1.81   35 SL-CA127   1.0   1.07   68.7   1.63   73.0   83.0   1.49   66.6   7.61   2.6		33SL-CA125		1.0		42.0	0.81	37.0	68.0	0.47	22.0	<u></u>
1 1D 41 1.49 166.6 17.61 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		34 SL-CA126				64.0	1.17	52.0	67.0	0.55	18.0	
Vew: Clinical Trial Data		3515 -CA127	9	9	797	289	163	730	830	1 49	9 99	26.
DIOC (DIII INCHINA CARACTER)			N in	C local	9,5			,	4000			
			See See		210			Kine cene	AURDZ	Ì		7

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7G. 3

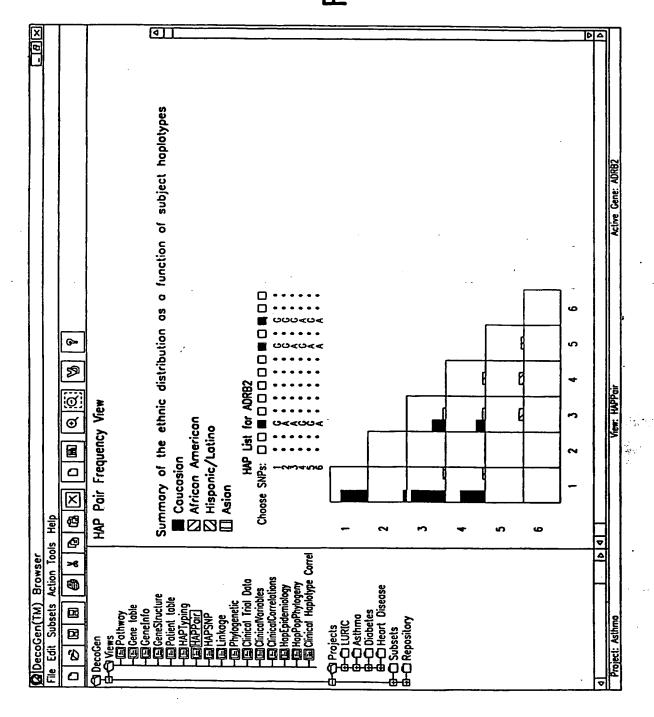


FIG. 32

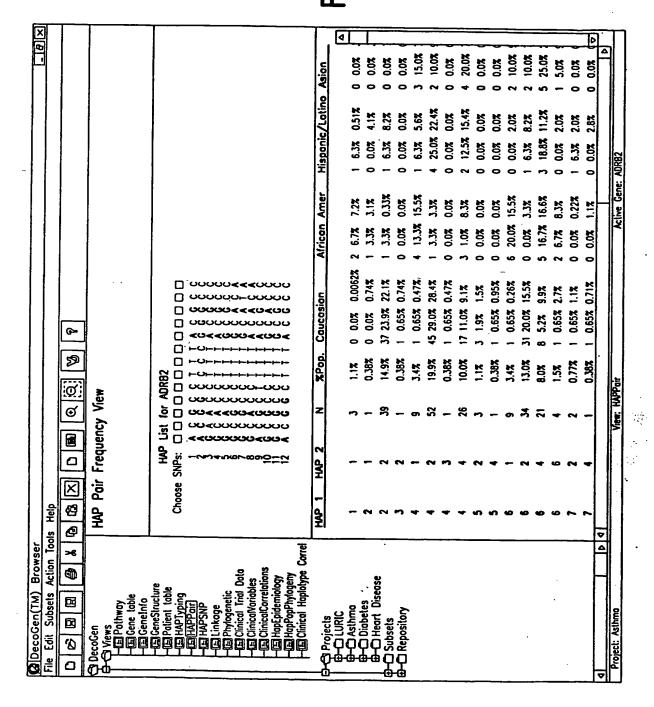
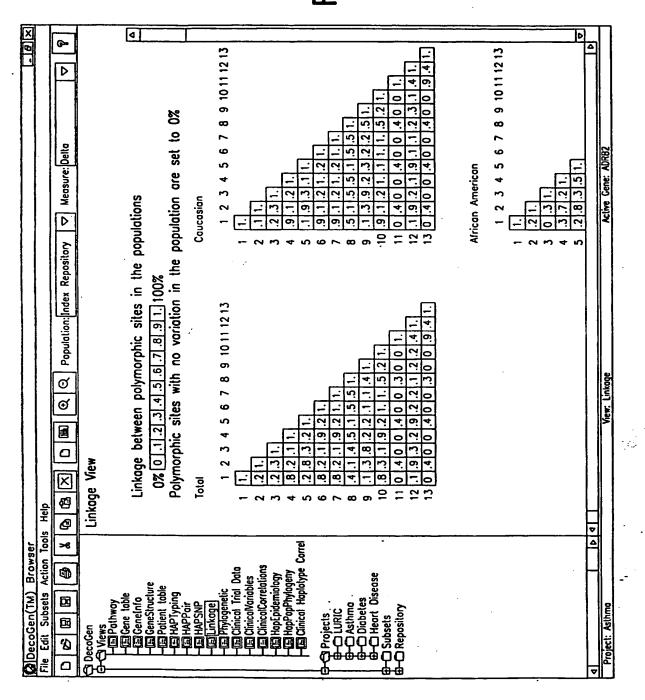
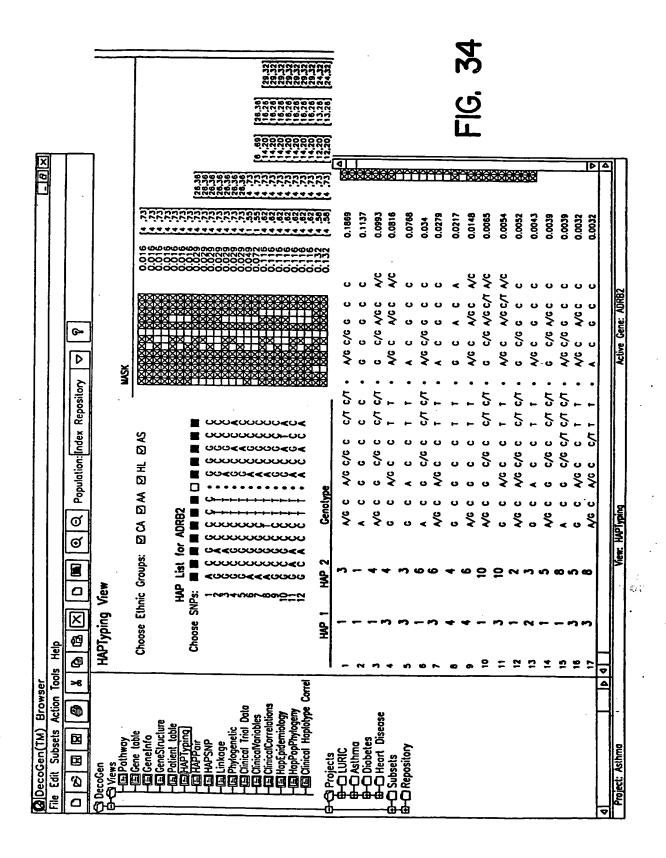


FIG. 3

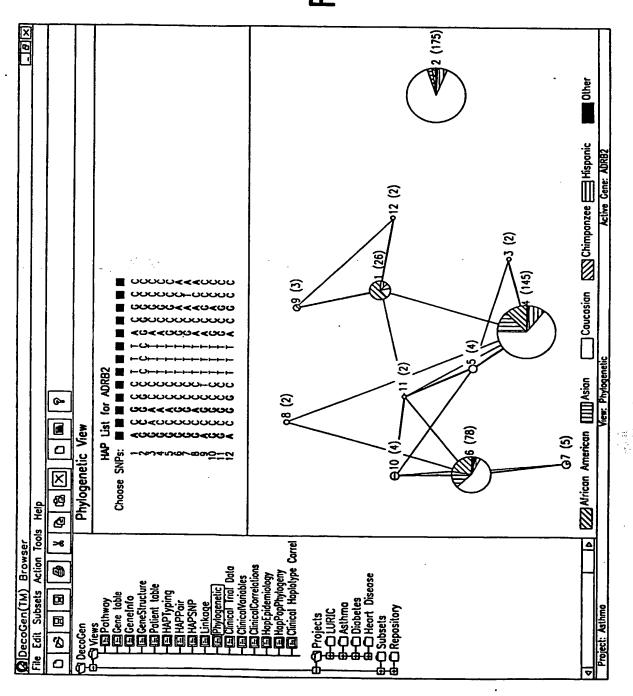


SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

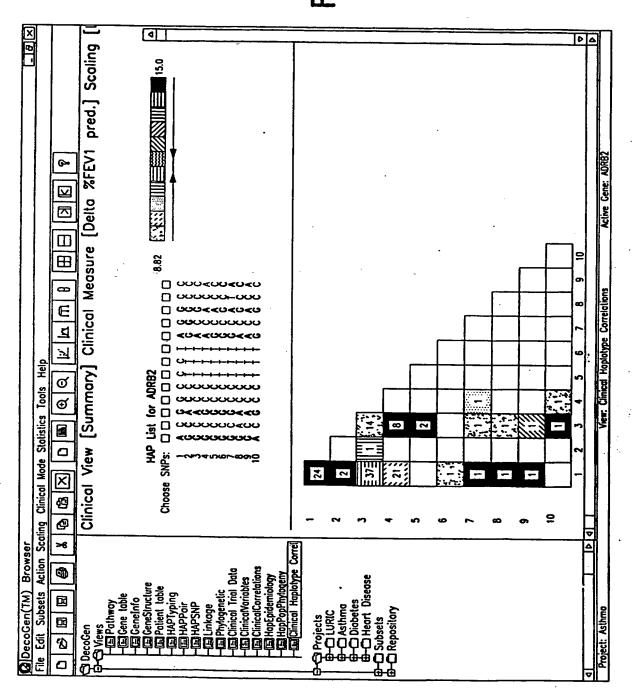
FIG. 35



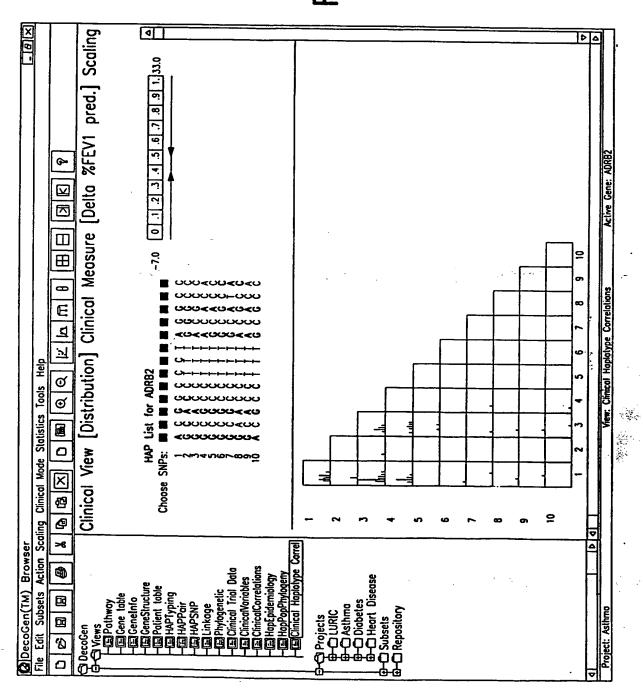
£.

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FIG. 36



**-1**G. 3:



SUBSTITUTE SHEET (RULE 26)

PCT/US00/17540

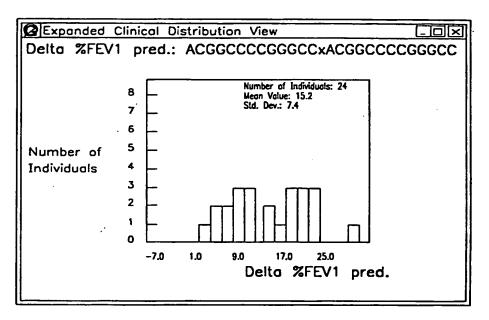


FIG. 38

DecoGen Single Ge	ene Statistics	Calculato	r				<u>.</u>	
File								
Show/Hide	CC Line							
Gene: adrenergic,	beta-2-,	receptor,	surface			ure: Delta %	FEV1 pr	ed.
			Confidence:	0.05 0.1	Fixed Si	ite: <u>-4</u>		
Regression Res	uits							님
Marker	Intercept	Slope	Stope Ran	ige	R** 2	Corr. Coef (R)	P-value	
+G+++++++	10.501	1.99	-0.08	4.06	0.0301	0.1734	0.0297	- 11
G	10.526	1.956	-0.11	4.02	0.0293	0.1711	0.0314	
□*******A+G**	14.583	-2.206	-4.28	-0.13	0.0365	-0.1911	0.0187	- 11
□**A****A****	14.471	-2.048	-4.13	0.032	0.0315	-0.1774	0.0268	-
□**A******G**	14.626	-2.241	-4.32	-0.16	0.0374	-0.1934	0.0175	- 11
□**A*****A*G**	14.615	-2.308	-4.4	-0.21 ~	0.0391	-0.1977	0.0156	11
□GCACCTTTACGCC	14.6	-2.343	-4.46	-0.22	0.0394	-0.1984	0.0153	- 11
								- 11
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FIG. 39A

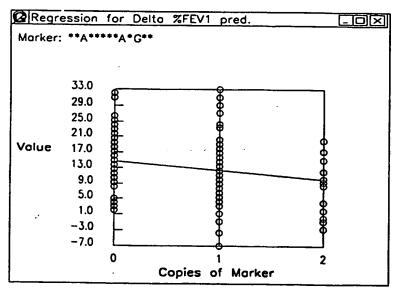
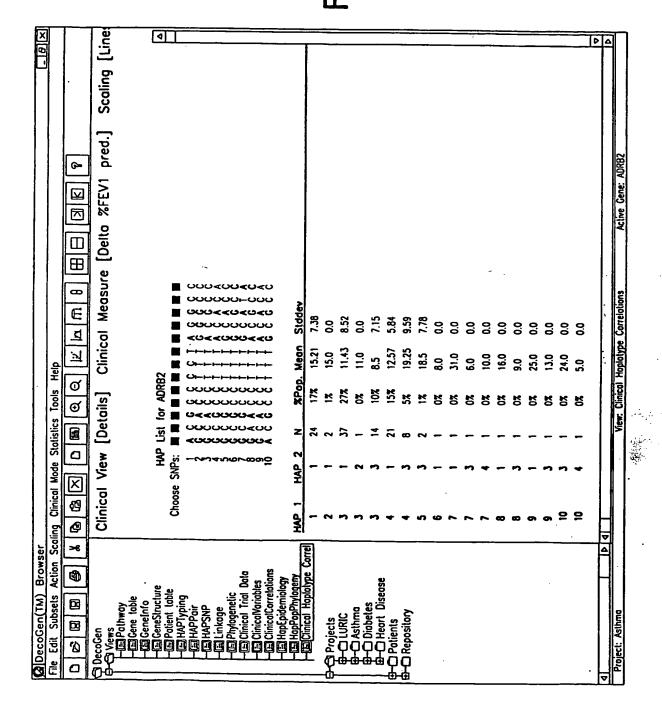


FIG. 39B

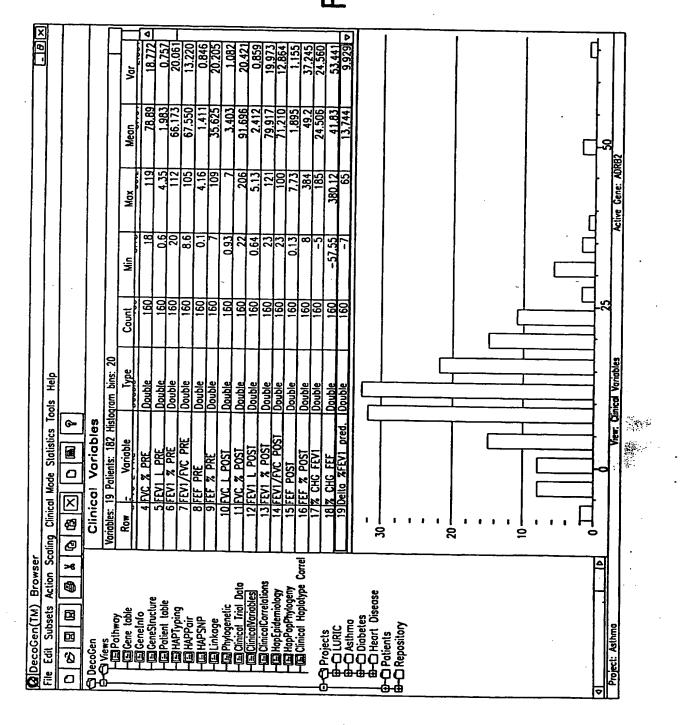
FIG. 40



DecoGen	Single Ger	ne Statistics	Calculator			[_ID]×
File				-		
<u>a</u> Q Q						
	<u> </u>					·
Clinical M	eosureme	ints ANOVA	Calculation	on		
1						
Source of			Squares F	-ratio		9
Between Gr			145.83	2.49		
Within Grou	ps	101	58.59			
P-value fo	r significonc	e: 0.027			•	
	146 15-14					
Choose SNI	HAP List for	r ADRB2				
0110036 3141		<u> </u>	GGGCC		-	
	3 G C A	11133	3 2 3 3 3 §			
	\$ 6 6 6	11133	33433			
	7 6 6 6	**************************************				
	CORPORATIONS CONTRACTORS CONTR	**************************************				
HAP 1	HAP 2	CCIII	ACGCC N	Averes	Std. Dev.	
	1		24	15.21	7.38	
	· 3		2 37	15.0	0.0	
i	4		21	11.4 <b>3</b> 12.57	5.84	
3	3		14	8.5	7.15	
3	4		8	19.25		
3	5		2	18.5	7.78	1
•			<del></del>			
						10

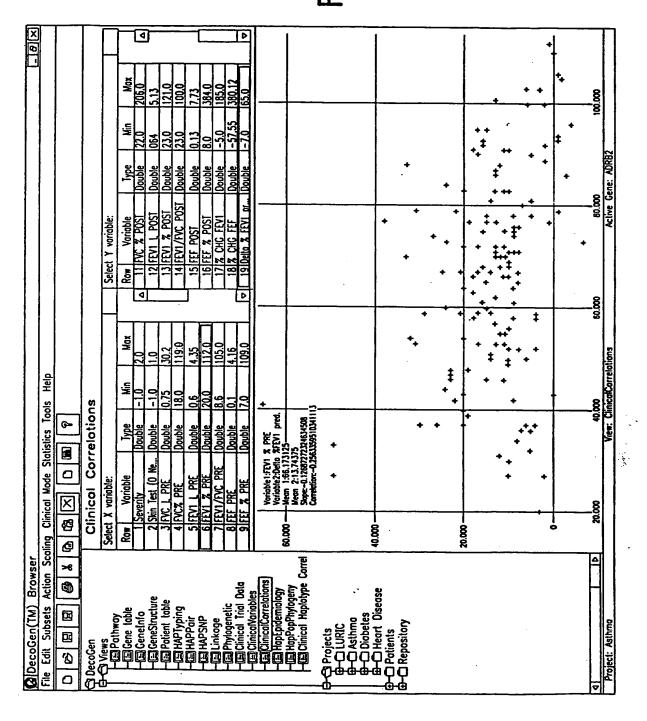
FIG. 41

FIG. 42

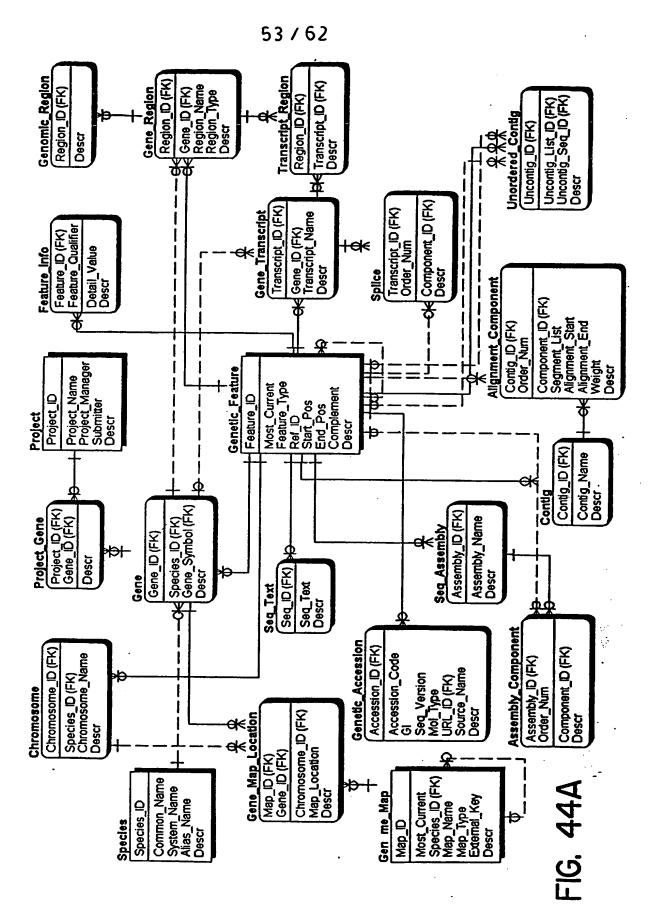


**SUBSTITUTE SHEET (RULE 26)** 

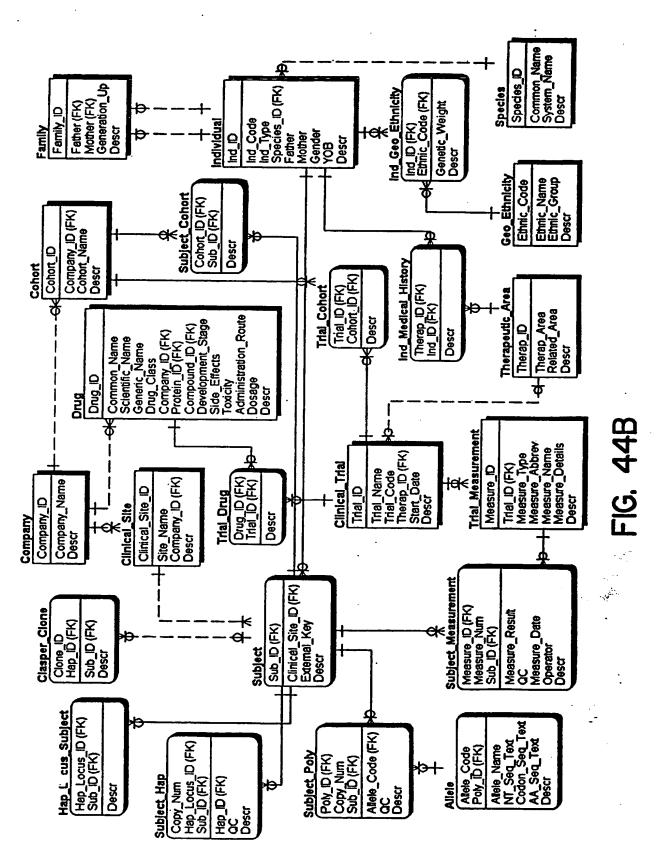
FIG. 4:



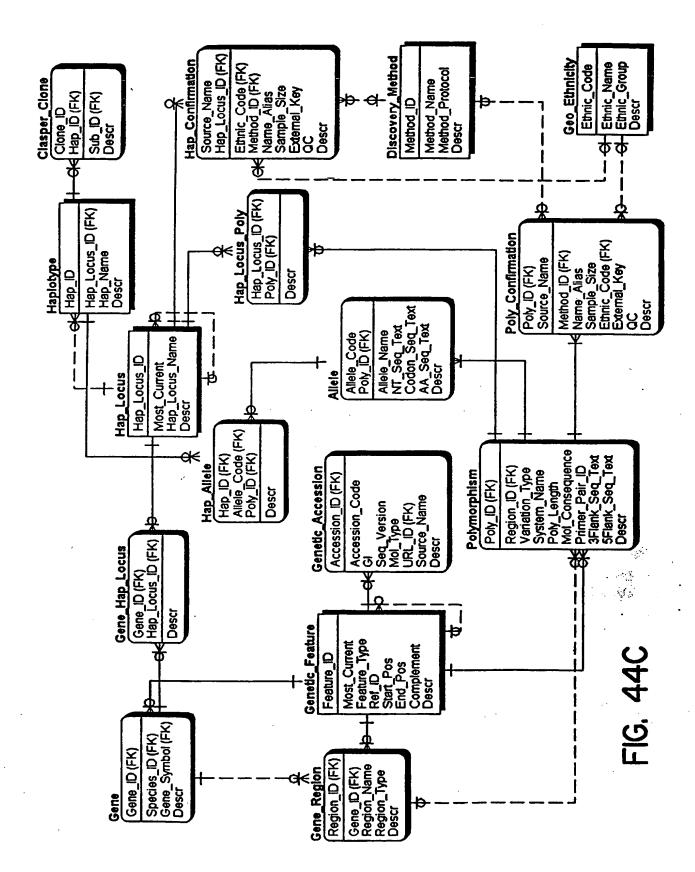
SUBSTITUTE SHEET (RULE 26)



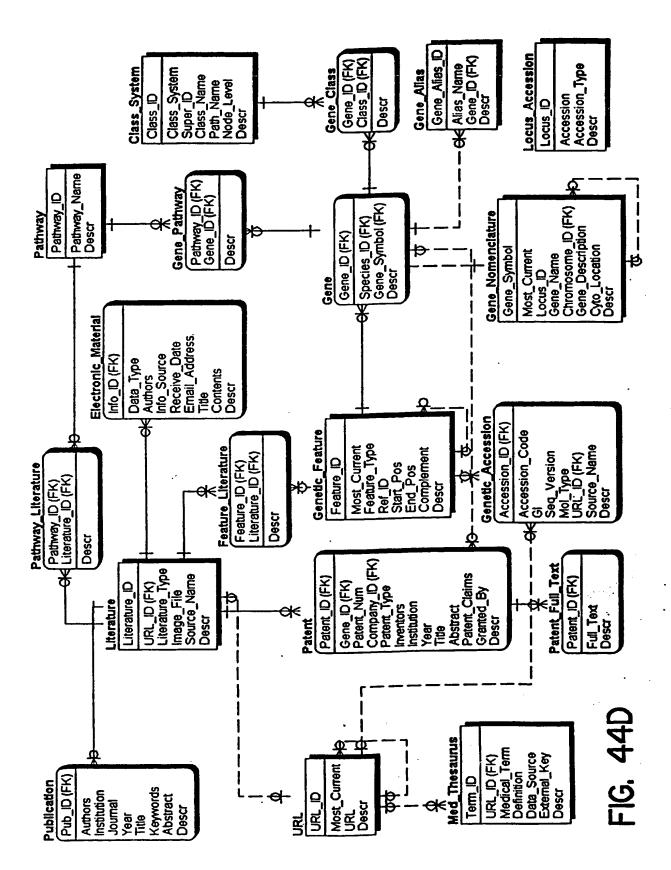
SUBSTITUTE SHEET (RULE 26)



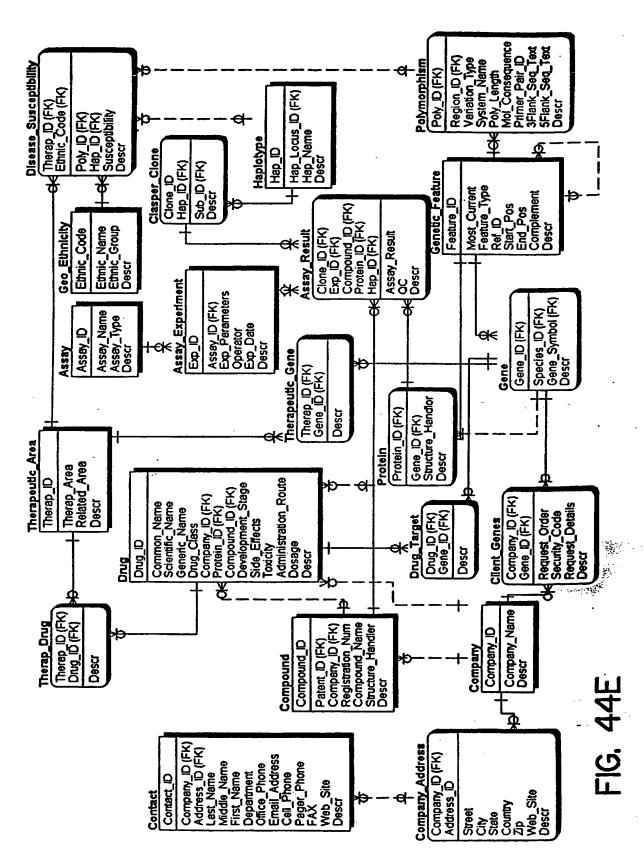
SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

### Legend of Figures:



ample 2

Rectangle Boxes: Tables in the database.

Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: | Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: | Karaman | Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 8: +---- Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.
- 10: | Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 12: --- Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.
- 14: \(\begin{align\*}
  \to --- \infty \\
  \text{Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.}\)

# FIG. 44F

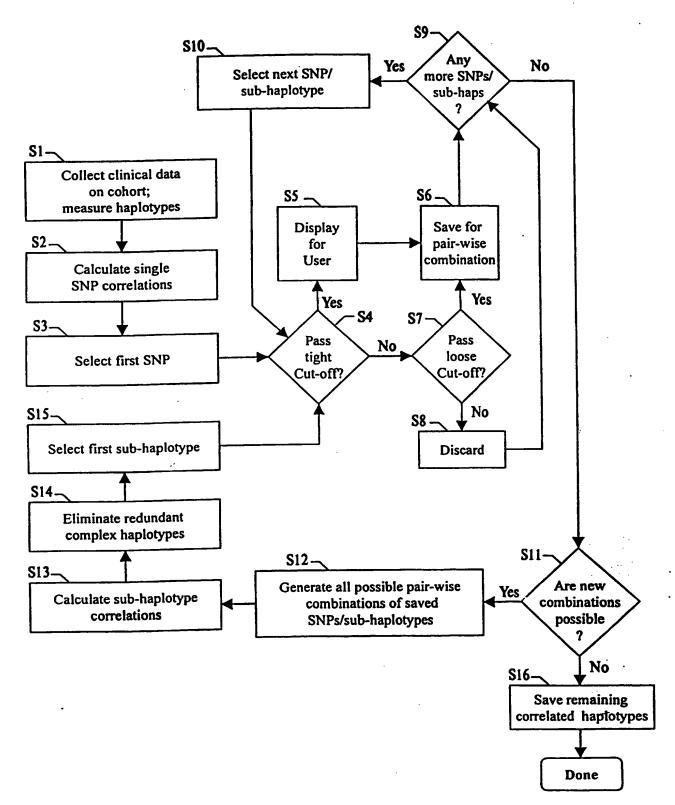


FIG. 45
SUBSTITUTE SHEET (RULE 26)

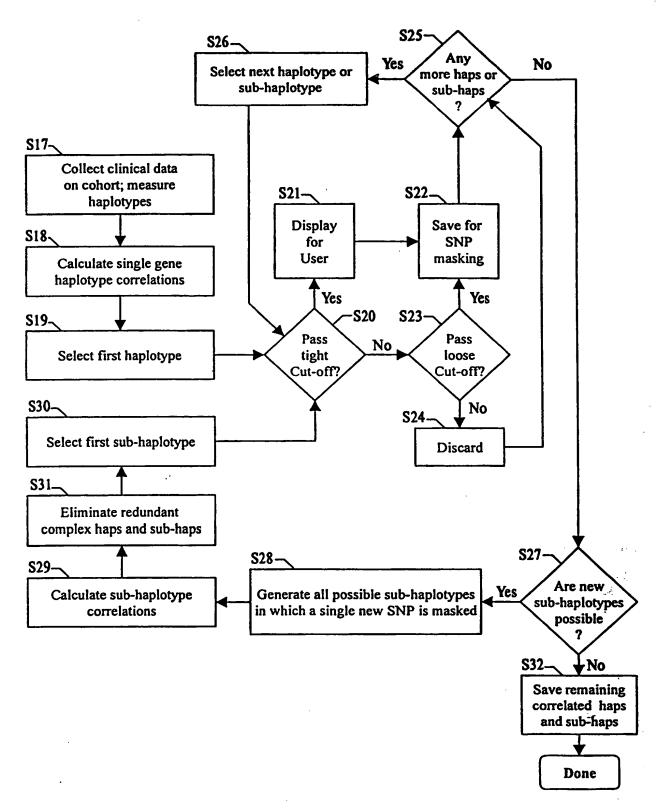
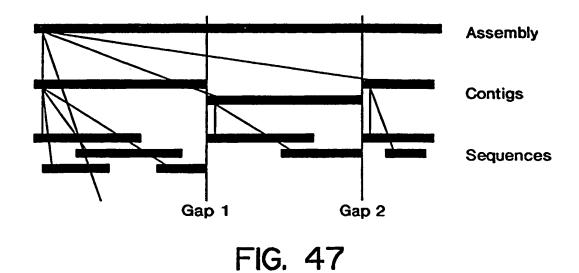


FIG. 46

SUBSTITUTE SHEET (RULE 26)



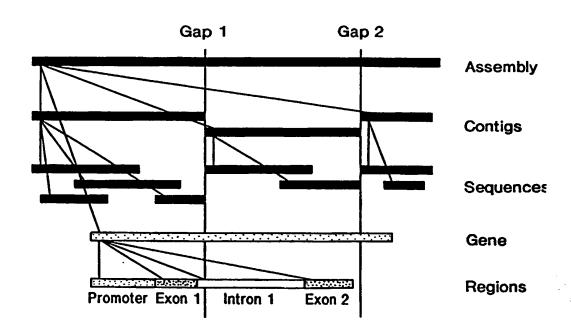


FIG. 48

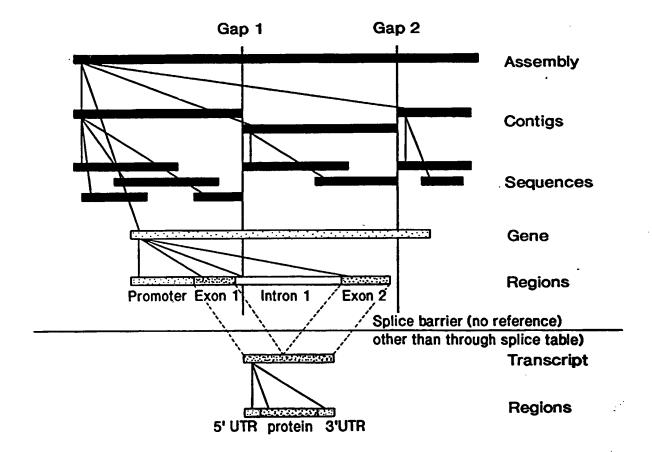


FIG. 49